



SEQUENCE LISTING

<110> Duvick, Johnathan P.

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Rao, Aragula Gururaj

Crasta, Oswald R.

Folkerts, Otto

<120> Amino Polyol Aamine Oxidase Polynucleotides and Related Polypeptides and Methods of Use

<130> 1134R

<140> US 09/658,835

<41> 2000-09-08

<150> US 60/092,936

<151> 1998-07-25

<150> US 60/135,391

<151> 1999-05-21

<150> US 09/352,159

<151> 1999-07-12

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<150> US 09/352,168

<151> 1999-07-12

<160> 54

<170> PatentIn version 3.1

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<213> *Exophiala spinifera*

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ggaggacgcc cgagaagcct tgttcgcgcc accacggcct gtcccatatc aagactatct 240
tgctatagta gcccaggata gaattttccg ccaatgcttg cttctcggcg ggaagaggtg 300
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<212> DNA

<213> Artificial Sequence

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<400> 3
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Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu	
20 25 30	
gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg ggt	144
Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly	
35 40 45	
ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat gac	192
Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp	
50 55 60	
agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag	240
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65 70 75 80	
ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa gac	288
Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp	
85 90 95	
ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag gag	336
Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu	
100 105 110	
gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc	384
Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile	
115 120 125	
gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag cgg	432
Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg	
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ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac ttg	480
Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu	
145 150 155 160	
cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc ggt	528
Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly	
165 170 175	
gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc aag	576
Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys	
180 185 190	
agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc ggg	624
Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly	

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225					230					235					240		
gaa	att	gag	cag	tcg	gca	tcc	ggc	tgt	aca	gta	cga	tcg	gcc	tcg	ggc	768	
Glu	Ile	Glu	Gln	Ser	Ala	Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser	Gly		
245					250					255							
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Ala	Val	Phe	Arg	Ser	Lys	Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr	Leu		
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Tyr	Pro	Thr	Leu	Thr	Phe	Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln	Ala		
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Leu	Ala	Glu	Asn	Ser	Ile	Leu	Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe	Val		
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Trp	Asp	Lys	Pro	Trp	Trp	Arg	Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu	Gln		
305					310					315					320		
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Ser	Ser	Cys	Asp	Pro	Ile	Ser	Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp	Val		
325					330					335							
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Asp	Arg	Gln	Trp	Ser	Ile	Thr	Cys	Phe	Met	Val	Gly	Asp	Pro	Gly	Arg		
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Lys	Trp	Ser	Gln	Gln	Ser	Lys	Gln	Val	Arg	Gln	Lys	Ser	Val	Trp	Asp		
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caa	ctc	cgc	gca	gcc	tac	gag	aac	gcc	ggg	gcc	caa	gtc	cca	gag	ccg	1152	
Gln	Leu	Arg	Ala	Ala	Tyr	Glu	Asn	Ala	Gly	Ala	Gln	Val	Pro	Glu	Pro		
370					375					380							
gcc	aac	gtg	ctc	gaa	atc	gag	tgg	tcg	aag	cag	cag	tat	ttc	caa	gga	1200	
Ala	Asn	Val	Leu	Glu	Ile	Glu	Trp	Ser	Lys	Gln	Gln	Tyr	Phe	Gln	Gly		
385					390					395					400		
gct	ccg	agc	gcc	gtc	tat	ggg	ctg	aac	gat	ctc	atc	aca	ctg	ggg	tcg	1248	
Ala	Pro	Ser	Ala	Val	Tyr	Gly	Leu	Asn	Asp	Leu	Ile	Thr	Leu	Gly	Ser		
405					410					415							
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Ala	Leu	Arg	Thr	Pro	Phe	Lys	Ser	Val	His	Phe	Val	Gly	Thr	Glu	Thr		
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tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt caa 1344
 Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln
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cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag 1389
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<211> 462

<212> PRT

<213> Exophiala spinifera

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 35 40 45

Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp
 50 55 60

Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu
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Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp
 85 90 95

Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu
 100 105 110

Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile
 115 120 125

Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg
 130 135 140

Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu
 145 150 155 160

Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly
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Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys
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 210 215 220

Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala
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Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala
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 325 330 335

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 340 345 350

Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp
 355 360 365

Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro
 370 375 380

Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly
 385 390 395 400

Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser
 405 410 415

Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr
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Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu	
20 25 30	
gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg ggt	144
Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly	
35 40 45	
ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat gac	192
Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp	
50 55 60	
agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag	240
Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu	
65 70 75 80	
ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa gac	288
Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp	
85 90 95	
ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag gag	336
Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu	
100 105 110	
gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc	384
Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile	
115 120 125	
gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag cgg	432
Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg	
130 135 140	
ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac ttg	480
Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu	
145 150 155 160	
cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc ggt	528
Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly	
165 170 175	
gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc aag	576
Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys	
180 185 190	
agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc ggg	624

Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly	
195 200 205	
cag tat gtg cga tgc aaa aca ggtgcgtgtg gtgtcgtctc aggtggggga	675
Gln Tyr Val Arg Cys Lys Thr	
210 215	
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Gly Met Gln Ser Ile Cys His Ala Met Ser	
220 225	
aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc gct gaa	776
Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu	
230 235 240	
att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc	824
Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala	
245 250 255	
gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc ttg tat	872
Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr	
260 265 270	
ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa gca ttg	920
Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu	
275 280 285	
gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc gta tgg	968
Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp	
290 295 300 305	
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Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser	
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Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp	
325 330 335	
cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga cgg aag	1112
Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys	
340 345 350	
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ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg gcc	1208
Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala	
370 375 380 385	
aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa gga gct	1256
Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala	
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ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt tcg gcg	1304
Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala	

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ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag acg tct			1352
Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser			
420	425	430	
tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt caa cga			1400
Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg			
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<211> 462

<212> PRT

<213> *Exophiala spinifera*

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35 40 45

Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp
50 55 60

Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu
65 70 75 80

Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp
85 90 95

Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu
100 105 110

Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile
115 120 125

Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg
 130 135 140

Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu
 145 150 155 160

Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly
 165 170 175

Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys
 180 185 190

Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly
 195 200 205

Gln Tyr Val Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met
 210 215 220

Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala
 225 230 235 240

Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly
 245 250 255

Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu
 260 265 270

Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala
 275 280 285

Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val
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Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln
 305 310 315 320

Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val
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Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg
 340 345 350

Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp
 355 360 365

Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro
 370 375 380

Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly
 385 390 395 400

Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser
 405 410 415

Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr
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Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln
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<210> 9

<211> 458

<212> PRT

<213> *Exophiala spinifera*

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Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly
 35 40 45

Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp
 50 55 60

Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu
 65 70 75 80

Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp
 85 90 95

Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu
 100 105 110

Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile
 115 120 125

Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg
 130 135 140

Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu
 145 150 155 160

Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly
 165 170 175

Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys
 180 185 190

Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly
 195 200 205

Gln Tyr Val Arg Cys Lys Thr Gly Ala Cys Gly Val Val Ser Gly Gly
 210 215 220

Gly Leu Val Ser Gln Trp Ser Phe Gln Val Cys Ser Arg Phe Ala Met
 225 230 235 240

Pro Cys Gln Arg Asn Leu Phe Gln Ala Gln Cys Thr Ser Thr Pro Pro
 245 250 255

Ser Leu Lys Leu Ser Ser Arg His Pro Ala Val Gln Tyr Asp Arg Pro
 260 265 270

Arg Ala Pro Cys Ser Glu Ala Lys Arg Trp Trp Phe Arg Tyr Arg Gln
 275 280 285

Pro Cys Ile Pro Pro His Phe His His Leu Phe Pro Pro Arg Ser Lys

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Gly Thr Ser Arg Gly Gly Ala Asn Lys Ala Ser Arg Ala Ser Ser Asn 325 330 335		
Arg Ala Val Thr Pro Ser His Leu Pro Glu Ile Pro Ala Ser Thr Ser 340 345 350		
Ile Asp Asn Gly Pro Leu Pro Val Ser Trp Ser Glu Thr Arg Asp Gly 355 360 365		
Ser Gly Pro Asn Ser Pro Ser Arg Tyr Asp Lys Ser Leu Ser Gly Thr 370 375 380		
Asn Ser Ala Gln Pro Thr Arg Thr Pro Gly Pro Lys Ser Gln Ser Arg 385 390 395 400		
Pro Thr Cys Ser Lys Ser Ser Gly Arg Ser Ser Ser Ile Ser Lys Glu 405 410 415		
Leu Arg Ala Pro Ser Met Gly Thr Ile Ser Ser His Trp Val Arg Arg 420 425 430		
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<211> 1392

<212> DNA

<213> *Exophiala spinifera*

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<222> (1)..(1389)

<223>

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<222> (1)..(3)

<223> Extra lysine in K:trAPAO

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Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly
1          5          10          15

ttg gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt      96
Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val
          20          25          30

ctt gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg     144
Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser
          35          40          45

ggt ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat     192
Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn
          50          55          60

gac agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg     240
Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu
        65          70          75          80

gag ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa     288
Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln
          85          90          95

gac ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag     336
Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu
          100          105          110

gag gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg     384
Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu
          115          120          125

atc gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag     432
Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys
          130          135          140

cgg ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac     480
Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn
          145          150          155          160
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ttg cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc	528
Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu	
165 170 175	
ggt gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc	576
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile	
180 185 190	
aag agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc	624
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly	
195 200 205	
ggg cag tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc	672
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala	
210 215 220	
atg tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc	720
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val	
225 230 235 240	
gct gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg	768
Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser	
245 250 255	
ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc	816
Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr	
260 265 270	
ttg tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa	864
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln	
275 280 285	
gca ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc	912
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe	
290 295 300	
gta tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc	960
Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu	
305 310 315 320	
caa tcg agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac	1008
Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp	
325 330 335	
gtc gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga	1056
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly	
340 345 350	
cgg aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg	1104
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp	
355 360 365	
gac caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag	1152
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu	
370 375 380	
ccg gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa	1200

Pro	Ala	Asn	Val	Leu	Glu	Ile	Glu	Trp	Ser	Lys	Gln	Gln	Tyr	Phe	Gln		
385					390					395					400		
gga	gct	ccg	agc	gcc	gtc	tat	ggg	ctg	aac	gat	ctc	atc	aca	ctg	ggt		1248
Gly	Ala	Pro	Ser	Ala	Val	Tyr	Gly	Leu	Asn	Asp	Leu	Ile	Thr	Leu	Gly		
				405					410					415			
tcg	gcg	ctc	aga	acg	ccg	ttc	aag	agt	gtt	cat	ttc	gtt	gga	acg	gag		1296
Ser	Ala	Leu	Arg	Thr	Pro	Phe	Lys	Ser	Val	His	Phe	Val	Gly	Thr	Glu		
				420					425					430			
acg	tct	tta	gtt	tgg	aaa	ggg	tat	atg	gaa	ggg	gcc	ata	cga	tcg	ggt		1344
Thr	Ser	Leu	Val	Trp	Lys	Gly	Tyr	Met	Glu	Gly	Ala	Ile	Arg	Ser	Gly		
				435				440					445				
caa	cga	ggt	gct	gca	gaa	gtt	gtg	gct	agc	ctg	gtg	cca	gca	gca	tag		1392
Gln	Arg	Gly	Ala	Ala	Glu	Val	Val	Ala	Ser	Leu	Val	Pro	Ala	Ala			
				450				455				460					

<210> 11

<211> 463

<212> PRT

<213> Exophiala spinifera

<220>

<221> misc_feature

<222> (1)..(3)

<223> Extra lysine in K:trAPAO

<400> 11

Lys	Asp	Asn	Val	Ala	Asp	Val	Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly	
1				5					10					15		
Leu	Glu	Thr	Ala	Arg	Lys	Val	Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	
			20					25					30			
Leu	Glu	Ala	Met	Asp	Arg	Val	Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	
		35					40					45				
Gly	Pro	Gly	Arg	Thr	Thr	Ile	Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	
	50					55					60					
Asp	Ser	Asn	Gln	Ser	Glu	Val	Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu	

65		70		75		80
Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln						
		85		90		95
Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu						
		100		105		110
Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu						
		115		120		125
Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys						
		130		135		140
Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn						
		145		150		155
Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu						
		165		170		175
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile						
		180		185		190
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly						
		195		200		205
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala						
		210		215		220
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val						
		225		230		235
Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser						
		245		250		255
Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr						
		260		265		270
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln						
		275		280		285
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe						
		290		295		300

Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu
305 310 315 320

Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp
325 330 335

Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly
340 345 350

Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp
355 360 365

Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu
370 375 380

Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln
385 390 395 400

Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly
405 410 415

Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu
420 425 430

Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly
435 440 445

Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
450 455 460

<210> 12

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer sequence designed for cloning DNA into expression vectors,
N23256

<400> 12
ggggaattca aagacaacgt tgcggacgtg gtag 34

<210> 13

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer sequence designed for cloning DNA into expression vectors
N23256

<400> 13
ggggcggccg cctatgctgc tggcaccagg ctag 34

<210> 14

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide for 3' RACE, N21965

<400> 14
tggtttcggtt accgacaacc ttgtatccc 29

<210> 15

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide for 5' RACE, N21968

<400> 15
gagttggtcc cagacagact tttgtcgt 28

<210> 16
 <211> 1673
 <212> DNA
 <213> *Exophiala spinifera*

<220>
 <221> sig_peptide
 <222> (1)..(267)
 <223> yeast alpha mating factor secretion signal

<220>
 <221> CDS
 <222> (1)..(1662)
 <223>

<400> 16
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 Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala Ser Ser
 1 5 10 15
 gca tta gct gct cca gtc aac act aca aca gaa gat gaa acg gca caa 96
 Ala Leu Ala Ala Pro Val Asn Thr Thr Thr Glu Asp Glu Thr Ala Gln
 20 25 30
 att ccg gct gaa gct gtc atc ggt tac tca gat tta gaa ggg gat ttc 144
 Ile Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp Phe
 35 40 45
 gat gtt gct gtt ttg cca ttt tcc aac agc aca aat aac ggg tta ttg 192
 Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu
 50 55 60
 ttt ata aat act act att gcc agc att gct gct aaa gaa gaa ggg gta 240
 Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val
 65 70 75 80
 tct ctc gag aaa aga gag gct gaa gct gaa ttc aaa gac aac gtt gcg 288
 Ser Leu Glu Lys Arg Glu Ala Glu Ala Glu Phe Lys Asp Asn Val Ala
 85 90 95

gac gtg gta gtg gtg ggc gct ggc ttg agc ggt ttg gag acg gca cgc Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg 100 105 110	336
aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp 115 120 125	384
cgt gta ggg gga aag act ctg agc gta caa tcg ggt ccc ggc agg acg Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr 130 135 140	432
act atc aac gac ctc ggc gct gcg tgg atc aat gac agc aac caa agc Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser 145 150 155 160	480
gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag ggc gag ctc cag Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln 165 170 175	528
agg acg act gga aat tca atc cat caa gca caa gac ggt aca acc act Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr 180 185 190	576
aca gct cct tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala 195 200 205	624
ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser 210 215 220	672
ctt caa gac ctc aag gcg agc cct cag gcg aag cgg ctc gac agt gtg Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val 225 230 235 240	720
agc ttc gcg cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu 245 250 255	768
ggc gta gca aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His 260 265 270	816
gag atc agc atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly 275 280 285	864
ctc agt aat att ttc tcg gac aag aaa gac ggc ggg cag tat atg cga Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg 290 295 300	912
tgc aaa aca ggt atg cag tcg att tgc cat gcc atg tca aag gaa ctt Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu 305 310 315 320	960
gtt cca ggc tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag	1008

Val	Pro	Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val	Ala	Glu	Ile	Glu	Gln	
				325					330					335		
tcg	gca	tcc	ggc	tgt	aca	gta	cga	tcg	gcc	tcg	ggc	gcc	gtg	ttc	cga	1056
Ser	Ala	Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser	Gly	Ala	Val	Phe	Arg	
			340					345					350			
agc	aaa	aag	gtg	gtg	gtt	tcg	tta	ccg	aca	acc	ttg	tat	ccc	acc	ttg	1104
Ser	Lys	Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr	Leu	Tyr	Pro	Thr	Leu	
		355					360					365				
aca	ttt	tca	cca	cct	ctt	ccc	gcc	gag	aag	caa	gca	ttg	gcg	gaa	aat	1152
Thr	Phe	Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln	Ala	Leu	Ala	Glu	Asn	
	370					375					380					
tct	atc	ctg	ggc	tac	tat	agc	aag	ata	gtc	ttc	gta	tgg	gac	aag	ccg	1200
Ser	Ile	Leu	Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe	Val	Trp	Asp	Lys	Pro	
385					390				395						400	
tgg	tgg	cgc	gaa	caa	ggc	ttc	tcg	ggc	gtc	ctc	caa	tcg	agc	tgt	gac	1248
Trp	Trp	Arg	Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu	Gln	Ser	Ser	Cys	Asp	
			405					410						415		
ccc	atc	tca	ttt	gcc	aga	gat	acc	agc	atc	gac	gtc	gat	cga	caa	tgg	1296
Pro	Ile	Ser	Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp	Val	Asp	Arg	Gln	Trp	
			420				425					430				
tcc	att	acc	tgt	ttc	atg	gtc	gga	gac	ccg	gga	cgg	aag	tgg	tcc	caa	1344
Ser	Ile	Thr	Cys	Phe	Met	Val	Gly	Asp	Pro	Gly	Arg	Lys	Trp	Ser	Gln	
		435				440						445				
cag	tcc	aag	cag	gta	cga	caa	aag	tct	gtc	tgg	gac	caa	ctc	cgc	gca	1392
Gln	Ser	Lys	Gln	Val	Arg	Gln	Lys	Ser	Val	Trp	Asp	Gln	Leu	Arg	Ala	
	450					455					460					
gcc	tac	gag	aac	gcc	ggg	gcc	caa	gtc	cca	gag	ccg	gcc	aac	gtg	ctc	1440
Ala	Tyr	Glu	Asn	Ala	Gly	Ala	Gln	Val	Pro	Glu	Pro	Ala	Asn	Val	Leu	
465				470				475						480		
gaa	atc	gag	tgg	tcg	aag	cag	cag	tat	ttc	caa	gga	gct	ccg	agc	gcc	1488
Glu	Ile	Glu	Trp	Ser	Lys	Gln	Gln	Tyr	Phe	Gln	Gly	Ala	Pro	Ser	Ala	
			485					490						495		
gtc	tat	ggg	ctg	aac	gat	ctc	atc	aca	ctg	ggt	tcg	gcg	ctc	aga	acg	1536
Val	Tyr	Gly	Leu	Asn	Asp	Leu	Ile	Thr	Leu	Gly	Ser	Ala	Leu	Arg	Thr	
			500					505					510			
ccg	ttc	aag	agt	gtt	cat	ttc	gtt	gga	acg	gag	acg	tct	tta	gtt	tgg	1584
Pro	Phe	Lys	Ser	Val	His	Phe	Val	Gly	Thr	Glu	Thr	Ser	Leu	Val	Trp	
		515					520					525				
aaa	ggg	tat	atg	gaa	ggg	gcc	ata	cga	tcg	ggt	caa	cga	ggt	gct	gca	1632
Lys	Gly	Tyr	Met	Glu	Gly	Ala	Ile	Arg	Ser	Gly	Gln	Arg	Gly	Ala	Ala	
	530					535					540					
gaa	gtt	gtg	gct	agc	ctg	gtg	cca	gca	gca	taggcggccg	c					1673
Glu	Val	Val	Ala	Ser	Leu	Val	Pro	Ala	Ala							

545

550

<210> 17

<211> 554

<212> PRT

<213> Exophiala spinifera

<400> 17

Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala Ser Ser
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Ala Leu Ala Ala Pro Val Asn Thr Thr Thr Glu Asp Glu Thr Ala Gln
20 25 30

Ile Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp Phe
35 40 45

Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu
50 55 60

Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val
65 70 75 80

Ser Leu Glu Lys Arg Glu Ala Glu Ala Glu Phe Lys Asp Asn Val Ala
85 90 95

Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg
100 105 110

Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp
115 120 125

Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr
130 135 140

Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser
145 150 155 160

Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln
165 170 175

Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr
 180 185 190

Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala
 195 200 205

Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser
 210 215 220

Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val
 225 230 235 240

Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu
 245 250 255

Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His
 260 265 270

Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly
 275 280 285

Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg
 290 295 300

Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu
 305 310 315 320

Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln
 325 330 335

Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg
 340 345 350

Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu
 355 360 365

Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn
 370 375 380

Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro
 385 390 395 400

Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp
405 410 415

Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp
420 425 430

Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln
435 440 445

Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala
450 455 460

Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu
465 470 475 480

Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala
485 490 495

Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr
500 505 510

Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp
515 520 525

Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala
530 535 540

Glu Val Val Ala Ser Leu Val Pro Ala Ala
545 550

<210> 18

<211> 2079

<212> DNA

<213> Unknown

<220>

<223> GST:K:trAPAO 2079 for bacterial expression

<220>

<221> CDS

<222> (1)..(2076)

<223>

<220>

<221> misc_feature

<222> (1)..(687)

<223> gst fusion + polylinker

<220>

<221> misc_feature

<222> (688)..(2076)

<223> K:trAPAO

<220>

<221> misc_feature

<222> (688)..(690)

<223> Extra lysine

<400> 18

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Met	Ser	Pro	Ile	Leu	Gly	Tyr	Trp	Lys	Ile	Lys	Gly	Leu	Val	Gln	Pro	
1				5				10						15		

act	cga	ctt	ctt	ttg	gaa	tat	ctt	gaa	gaa	aaa	tat	gaa	gag	cat	ttg	96
Thr	Arg	Leu	Leu	Leu	Glu	Tyr	Leu	Glu	Glu	Lys	Tyr	Glu	Glu	His	Leu	
		20					25						30			

tat	gag	cgc	gat	gaa	ggt	gat	aaa	tgg	cga	aac	aaa	aag	ttt	gaa	ttg	144
Tyr	Glu	Arg	Asp	Glu	Gly	Asp	Lys	Trp	Arg	Asn	Lys	Lys	Phe	Glu	Leu	
		35				40						45				

ggt	ttg	gag	ttt	ccc	aat	ctt	cct	tat	tat	att	gat	ggt	gat	gtt	aaa	192
Gly	Leu	Glu	Phe	Pro	Asn	Leu	Pro	Tyr	Tyr	Ile	Asp	Gly	Asp	Val	Lys	
	50					55					60					

tta	aca	cag	tct	atg	gcc	atc	ata	cgt	tat	ata	gct	gac	aag	cac	aac	240
Leu	Thr	Gln	Ser	Met	Ala	Ile	Ile	Arg	Tyr	Ile	Ala	Asp	Lys	His	Asn	

65	70	75	80	
atg ttg ggt ggt tgt cca aaa gag cgt gca gag att tca atg ctt gaa				288
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu	85	90	95	
gga gcg gtt ttg gat att aga tac ggt gtt tcg aga att gca tat agt				336
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser	100	105	110	
aaa gac ttt gaa act ctc aaa gtt gat ttt ctt agc aag cta cct gaa				384
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu	115	120	125	
atg ctg aaa atg ttc gaa gat cgt tta tgt cat aaa aca tat tta aat				432
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn	130	135	140	
ggt gat cat gta acc cat cct gac ttc atg ttg tat gac gct ctt gat				480
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp	145	150	155	160
ggt gtt tta tac atg gac cca atg tgc ctg gat gcg ttc cca aaa tta				528
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu	165	170	175	
ggt tgt ttt aaa aaa cgt att gaa gct atc cca caa att gat aag tac				576
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr	180	185	190	
ttg aaa tcc agc aag tat ata gca tgg cct ttg cag gcc tgg caa gcc				624
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala	195	200	205	
acg ttt ggt ggt ggc gac cat cct cca aaa tcg gat ctg gtt ccg cgt				672
Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg	210	215	220	
gga tcc ccg gaa ttc aaa gac aac gtt gcg gac gtg gta gtg gtg gcc				720
Gly Ser Pro Glu Phe Lys Asp Asn Val Ala Asp Val Val Val Val Gly	225	230	235	240
gct gcc ttg agc ggt ttg gag acg gca cgc aaa gtc cag gcc gcc ggt				768
Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly	245	250	255	
ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta ggg gga aag act				816
Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr	260	265	270	
ctg agc gta caa tcg ggt ccc gcc agg acg act atc aac gac ctc gcc				864
Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly	275	280	285	
gct gcg tgg atc aat gac agc aac caa agc gaa gta tcc aga ttg ttt				912
Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe	290	295	300	

gaa aga ttt cat ttg gag ggc gag ctc cag agg acg act gga aat tca	960
Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser	
305 310 315 320	
atc cat caa gca caa gac ggt aca acc act aca gct cct tat ggt gac	1008
Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp	
325 330 335	
tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg gaa ctc ctc ccc	1056
Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro	
340 345 350	
gta tgg tct cag ctg atc gaa gag cat agc ctt caa gac ctc aag gcg	1104
Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala	
355 360 365	
agc cct cag gcg aag cgg ctc gac agt gtg agc ttc gcg cac tac tgt	1152
Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys	
370 375 380	
gag aag gaa cta aac ttg cct gct gtt ctc ggc gta gca aac cag atc	1200
Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile	
385 390 395 400	
aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc agc atg ctt ttt	1248
Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Leu Phe	
405 410 415	
ctc acc gac tac atc aag agt gcc acc ggt ctc agt aat att ttc tcg	1296
Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser	
420 425 430	
gac aag aaa gac ggc ggg cag tat atg cga tgc aaa aca ggt atg cag	1344
Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln	
435 440 445	
tcg att tgc cat gcc atg tca aag gaa ctt gtt cca ggc tca gtg cac	1392
Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val His	
450 455 460	
ctc aac acc ccc gtc gct gaa att gag cag tcg gca tcc ggc tgt aca	1440
Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr	
465 470 475 480	
gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt	1488
Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val Val Val	
485 490 495	
tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt tca cca cct ctt	1536
Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu	
500 505 510	
ccc gcc gag aag caa gca ttg gcg gaa aat tct atc ctg ggc tac tat	1584
Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr	
515 520 525	

agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg cgc gaa caa ggc	1632
Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly	
530 535 540	

ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc tca ttt gcc aga	1680
Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg	
545 550 555 560	

gat acc agc atc gac gtc gat cga caa tgg tcc att acc tgt ttc atg	1728
Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met	
565 570 575	

gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc aag cag gta cga	1776
Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg	
580 585 590	

caa aag tct gtc tgg gac caa ctc cgc gca gcc tac gag aac gcc ggg	1824
Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly	
595 600 605	

gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc gag tgg tcg aag	1872
Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys	
610 615 620	

cag cag tat ttc caa gga gct ccg agc gcc gtc tat ggg ctg aac gat	1920
Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp	
625 630 635 640	

ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc aag agt gtt cat	1968
Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His	
645 650 655	

ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg tat atg gaa ggg	2016
Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly	
660 665 670	

gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt gtg gct agc ctg	2064
Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu	
675 680 685	

gtg cca gca gca tag	2079
Val Pro Ala Ala	
690	

<210> 19

<211> 692

<212> PRT

<213> Unknown

<220>

<223> GST:K:trAPAO 2079 for bacterial expression

<220>

<221> misc_feature

<222> (1)..(687)

<223> gst fusion + polylinker

<220>

<221> misc_feature

<222> (688)..(2076)

<223> K:trAPAO

<220>

<221> misc_feature

<222> (688)..(690)

<223> Extra lysine

<400> 19

Met	Ser	Pro	Ile	Leu	Gly	Tyr	Trp	Lys	Ile	Lys	Gly	Leu	Val	Gln	Pro
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Thr	Arg	Leu	Leu	Leu	Glu	Tyr	Leu	Glu	Glu	Lys	Tyr	Glu	Glu	His	Leu
		20					25					30			

Tyr	Glu	Arg	Asp	Glu	Gly	Asp	Lys	Trp	Arg	Asn	Lys	Lys	Phe	Glu	Leu
	35					40					45				

Gly	Leu	Glu	Phe	Pro	Asn	Leu	Pro	Tyr	Tyr	Ile	Asp	Gly	Asp	Val	Lys
50					55					60					

Leu	Thr	Gln	Ser	Met	Ala	Ile	Ile	Arg	Tyr	Ile	Ala	Asp	Lys	His	Asn
65				70					75					80	

Met	Leu	Gly	Gly	Cys	Pro	Lys	Glu	Arg	Ala	Glu	Ile	Ser	Met	Leu	Glu
			85					90						95	

Gly	Ala	Val	Leu	Asp	Ile	Arg	Tyr	Gly	Val	Ser	Arg	Ile	Ala	Tyr	Ser
		100						105					110		

Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu

115	120	125
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn		
130	135	140
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp		
145	150	155 160
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu		
	165	170 175
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr		
	180	185 190
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala		
	195	200 205
Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg		
	210	215 220
Gly Ser Pro Glu Phe Lys Asp Asn Val Ala Asp Val Val Val Val Gly		
225	230	235 240
Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly		
	245	250 255
Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr		
	260	265 270
Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly		
	275	280 285
Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe		
	290	300
Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser		
305	310	315 320
Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp		
	325	330 335
Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro		
	340	345 350

Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala
 355 360 365

Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys
 370 375 380

Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile
 385 390 395 400

Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Leu Phe
 405 410 415

Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser
 420 425 430

Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln
 435 440 445

Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val His
 450 455 460

Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr
 465 470 475 480

Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val Val Val
 485 490 495

Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu
 500 505 510

Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr
 515 520 525

Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly
 530 535 540

Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg
 545 550 555 560

Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met
 565 570 575

Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg
580 585 590

Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly
595 600 605

Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys
610 615 620

Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp
625 630 635 640

Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His
645 650 655

Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly
660 665 670

Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu
675 680 685

Val Pro Ala Ala
690

<210> 20

<211> 1464

<212> DNA

<213> Unknown

<220>

<223> K:trAPAO translational fusion with barley alpha amylase

<220>

<221> sig_peptide

<222> (1)..(72)

<223> Barley alpha amylase signal sequence

<220>

<221> misc_feature

<222> (73)..(1464)

<223> K:trAPAO cDNA

<220>

<221> CDS

<222> (1)..(1461)

<223>

<220>

<221> misc_feature

<222> (73)..(75)

<223> Added lysine residue

<400> 20

atg gcc aac aag cac ctg agc ctc tcc ctc ttc ctc gtg ctc ctc ggc	48
Met Ala Asn Lys His Leu Ser Leu Ser Leu Phe Leu Val Leu Leu Gly	
1 5 10 15	

ctc tcc gcc tcc ctc gcc agc ggc aaa gac aac gtt gcg gac gtg gta	96
Leu Ser Ala Ser Leu Ala Ser Gly Lys Asp Asn Val Ala Asp Val Val	
20 25 30	

gtg gtg ggc gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc cag	144
Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln	
35 40 45	

gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta ggg	192
Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly	
50 55 60	

gga aag act ctg agc gta caa tcg ggt ccc ggc agg acg act atc aac	240
Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn	
65 70 75 80	

gac ctc ggc gct gcg tgg atc aat gac agc aac caa agc gaa gta tcc	288
Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser	
85 90 95	

aga ttg ttt gaa aga ttt cat ttg gag ggc gag ctc cag agg acg act	336
Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr	

100	105	110	
gga aat tca atc cat caa gca Gly Asn Ser Ile His Gln Ala	caa gac ggt aca acc act Gln Asp Gly Thr Thr Thr	aca gct cct Thr Ala Pro	384
115	120	125	
tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg gaa Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu			432
130	135	140	
ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc ctt caa gac Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp			480
145	150	155	160
ctc aag gcg agc cct cag gcg aag cgg ctc gac agt gtg agc ttc gcg Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala			528
165	170	175	
cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc ggc gta gca His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala			576
180	185	190	
aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc agc Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser			624
195	200	205	
atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt ctc agt aat Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn			672
210	215	220	
att ttc tcg gac aag aaa gac ggc ggg cag tat atg cga tgc aaa aca Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr			720
225	230	235	240
ggt atg cag tcg att tgc cat gcc atg tca aag gaa ctt gtt cca ggc Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly			768
245	250	255	
tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag tcg gca tcc Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser			816
260	265	270	
ggc tgt aca gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa aag Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys			864
275	280	285	
gtg gtg gtt tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt tca Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser			912
290	295	300	
cca cct ctt ccc gcc gag aag caa gca ttg gcg gaa aat tct atc ctg Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu			960
305	310	315	320
ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg cgc Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg			1008
325	330	335	

gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc tca	1056
Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser	
340 345 350	
ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg tcc att acc	1104
Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr	
355 360 365	
tgt ttc atg gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc aag	1152
Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys	
370 375 380	
cag gta cga caa aag tct gtc tgg gac caa ctc cgc gca gcc tac gag	1200
Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu	
385 390 395 400	
aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc gag	1248
Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu	
405 410 415	
tgg tcg aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat ggg	1296
Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly	
420 425 430	
ctg aac gat ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc aag	1344
Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys	
435 440 445	
agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg tat	1392
Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr	
450 455 460	
atg gaa ggg gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt gtg	1440
Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val	
465 470 475 480	
gct agc ctg gtg cca gca gca tag	1464
Ala Ser Leu Val Pro Ala Ala	
485	

<210> 21

<211> 487

<212> PRT

<213> Unknown

<220>

<223> K:trAPAO translational fusion with barley alpha amylase

<220>

<221> misc_feature

<222> (73)..(1464)

<223> K:trAPAO cDNA

<220>

<221> misc_feature

<222> (73)..(75)

<223> Added lysine residue

<400> 21

Met Ala Asn Lys His Leu Ser Leu Ser Leu Phe Leu Val Leu Leu Gly
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Leu Ser Ala Ser Leu Ala Ser Gly Lys Asp Asn Val Ala Asp Val Val
20 25 30

Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln
35 40 45

Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly
50 55 60

Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn
65 70 75 80

Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser
85 90 95

Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr
100 105 110

Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro
115 120 125

Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu
130 135 140

Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp
145 150 155 160

Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala
165 170 175

His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala
180 185 190

Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser
195 200 205

Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn
210 215 220

Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr
225 230 235 240

Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly
245 250 255

Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser
260 265 270

Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys
275 280 285

Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser
290 295 300

Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu
305 310 315 320

Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg
325 330 335

Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser
340 345 350

Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr
355 360 365

Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys
370 375 380

Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu

385 390 395 400

Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu
405 410 415

Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly
420 425 430

Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys
435 440 445

Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr
450 455 460

Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val
465 470 475 480

Ala Ser Leu Val Pro Ala Ala
485

<210> 22

<211> 1803

<212> DNA

<213> Exophiala spinifera

 $\langle 220 \rangle$

<221> CDS

<222> (1) .. (1800)

<223>

<400>	22															
atg gca ctt gca ccg agc tac atc aat ccc cca aac gtc gcc tcc cca																48
Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Val Ala Ser Pro																
1	5	10										15				
gca ggg tat tct cac gtc ggc gta ggc cca gac gga ggg agg tat gtg																96
gca ggg tat tct cac gtc ggc gta ggc cca gac gga ggg agg tat gtg																96
Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Gly Arg Tyr Val																
	20	25										30				
aca ata gct gga cag att gga caa gac gct tcg qgc qtg aca gac cct																144

Thr	Ile	Ala	Gly	Gln	Ile	Gly	Gln	Asp	Ala	Ser	Gly	Val	Thr	Asp	Pro		
		35					40					45					
gcc	tac	gag	aaa	cag	gtt	gcc	caa	gca	ttc	gcc	aat	ctg	cga	gct	tgc	192	
Ala	Tyr	Glu	Lys	Gln	Val	Ala	Gln	Ala	Phe	Ala	Asn	Leu	Arg	Ala	Cys		
	50					55					60						
ctt	gct	gca	gtt	gga	gcc	act	tca	aac	gac	gtc	acc	aag	ctc	aat	tac	240	
Leu	Ala	Ala	Val	Gly	Ala	Thr	Ser	Asn	Asp	Val	Thr	Lys	Leu	Asn	Tyr		
	65			70						75					80		
tac	atc	gtc	gac	tac	gcc	ccg	agc	aaa	ctc	acc	gca	att	gga	gat	ggg	288	
Tyr	Ile	Val	Asp	Tyr	Ala	Pro	Ser	Lys	Leu	Thr	Ala	Ile	Gly	Asp	Gly		
				85					90					95			
ctg	aag	gct	acc	ttt	gcc	ctt	gac	agg	ctc	cct	cct	tgc	acg	ctg	gtg	336	
Leu	Lys	Ala	Thr	Phe	Ala	Leu	Asp	Arg	Leu	Pro	Pro	Cys	Thr	Leu	Val		
			100					105					110				
cca	gtg	tcg	gcc	ttg	tct	tca	cct	gaa	tac	ctc	ttt	gag	gtt	gat	gcc	384	
Pro	Val	Ser	Ala	Leu	Ser	Ser	Pro	Glu	Tyr	Leu	Phe	Glu	Val	Asp	Ala		
			115				120						125				
acg	gcg	ctg	gtg	ccg	gga	cac	acg	acc	cca	gac	aac	gtt	gcg	gac	gtg	432	
Thr	Ala	Leu	Val	Pro	Gly	His	Thr	Thr	Pro	Asp	Asn	Val	Ala	Asp	Val		
	130					135					140						
gta	gtg	gtg	ggc	gct	ggc	ttg	agc	ggg	ttg	gag	acg	gca	cgc	aaa	gtc	480	
gta	gtg	gtg	ggc	gct	ggc	ttg	agc	ggg	ttg	gag	acg	gca	cgc	aaa	gtc	480	
Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly	Leu	Glu	Thr	Ala	Arg	Lys	Val		
	145				150					155					160		
cag	gcc	gcc	ggg	ctg	tcc	tgc	ctc	gtt	ctt	gag	gcg	atg	gat	cgt	gta	528	
Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	Leu	Glu	Ala	Met	Asp	Arg	Val		
				165					170					175			
ggg	gga	aag	act	ctg	agc	gta	caa	tcg	ggg	ccc	ggc	agg	acg	act	atc	576	
Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly	Pro	Gly	Arg	Thr	Thr	Ile		
			180					185					190				
aac	gac	ctc	ggc	gct	gcg	tgg	atc	aat	gac	agc	aac	caa	agc	gaa	gta	624	
Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp	Ser	Asn	Gln	Ser	Glu	Val		
		195					200					205					
tcc	aga	ttg	ttt	gaa	aga	ttt	cat	ttg	gag	ggc	gag	ctc	cag	agg	acg	672	
Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu	Glu	Gly	Glu	Leu	Gln	Arg	Thr		
	210					215					220						
act	gga	aat	tca	atc	cat	caa	gca	caa	gac	ggg	aca	acc	act	aca	gct	720	
Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	Asp	Gly	Thr	Thr	Thr	Thr	Ala		
	225				230					235					240		
cct	tat	ggg	gac	tcc	ttg	ctg	agc	gag	gag	gtt	gca	agt	gca	ctt	gcg	768	
Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	Glu	Val	Ala	Ser	Ala	Leu	Ala		
				245					250					255			
gaa	ctc	ctc	ccc	gta	tgg	tct	cag	ctg	atc	gaa	gag	cat	agc	ctt	caa	816	
Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu	Ile	Glu	Glu	His	Ser	Leu	Gln		

	260		265		270	
gac ctc aag gcg agc cct cag gcg aag cgg ctc gac agt gtg agc ttc						864
gac ctc aag gcg agc cct cag gcg aag cgg ctc gac agt gtg agc ttc						864
Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe						
	275		280		285	
gcg cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc ggc gta						912
Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val						
	290		295		300	
gca aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc						960
Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile						
	305		310		315	320
agc atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt ctc agt						1008
Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser						
	325		330		335	
aat att ttc tcg gac aag aaa gac ggc ggg cag tat atg cga tgc aaa						1056
Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys						
	340		345		350	
aca ggt atg cag tcg att tgc cat gcc atg tca aag gaa ctt gtt cca						1104
Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro						
	355		360		365	
ggc tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag tcg gca						1152
Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala						
	370		375		380	
tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa						1200
Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys						
	385		390		395	400
aag gtg gtg gtt tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt						1248
aag gtg gtg gtt tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt						1248
Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe						
	405		410		415	
tca cca cct ctt ccc gcc gag aag caa gca ttg gcg gaa aat tct atc						1296
Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile						
	420		425		430	
ctg ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg						1344
Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp						
	435		440		445	
cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc						1392
Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile						
	450		455		460	
tca ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg tcc att						1440
Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile						
	465		470		475	480
acc tgt ttc atg gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc						1488
Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser						
	485		490		495	

aag cag gta cga caa aag tct gtc tgg gac caa ctc cgc gca gcc tac 1536
 Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr
 500 505 510

gag aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc 1584
 Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile
 515 520 525

gag tgg tcg aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat 1632
 gag tgg tcg aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat 1632
 Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr
 530 535 540

ggg ctg aac gat ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc 1680
 Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe
 545 550 555 560

aag agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg 1728
 Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly
 565 570 575

tat atg gaa ggg gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt 1776
 Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val
 580 585 590

gtg gct agc ctg gtg cca gca gca tag 1803
 Val Ala Ser Leu Val Pro Ala Ala
 595 600

<210> 23

<211> 600

<212> PRT

<213> *Exophiala spinifera*

<400> 23

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 1 5 10 15

Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Gly Arg Tyr Val
 20 25 30

Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro
 35 40 45

Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys
 50 55 60

Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr
 65 70 75 80

Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly
 85 90 95

Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val
 100 105 110

Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala
 115 120 125

Thr Ala Leu Val Pro Gly His Thr Thr Pro Asp Asn Val Ala Asp Val
 130 135 140

Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val
 145 150 155 160

Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val
 165 170 175

Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile
 180 185 190

Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val
 195 200 205

Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr
 210 215 220

Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala
 225 230 235 240

Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala
 245 250 255

Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln
 260 265 270

Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe
 275 280 285

Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val
 290 295 300

Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile
 305 310 315 320

Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser
 325 330 335

Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys
 340 345 350

Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro
 355 360 365

Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala
 370 375 380

Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys
 385 390 395 400

Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe
 405 410 415

Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile
 420 425 430

Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp
 435 440 445

Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile
 450 455 460

Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile
 465 470 475 480

Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser
 485 490 495

Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr
 500 505 510

Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile

515					520					525						
Glu	Trp	Ser	Lys	Gln	Gln	Tyr	Phe	Gln	Gly	Ala	Pro	Ser	Ala	Val	Tyr	
530					535					540						
Gly	Leu	Asn	Asp	Leu	Ile	Thr	Leu	Gly	Ser	Ala	Leu	Arg	Thr	Pro	Phe	
545					550					555					560	
Lys	Ser	Val	His	Phe	Val	Gly	Thr	Glu	Thr	Ser	Leu	Val	Trp	Lys	Gly	
565					570					575						
Tyr	Met	Glu	Gly	Ala	Ile	Arg	Ser	Gly	Gln	Arg	Gly	Ala	Ala	Glu	Val	
580					585					590						
Val	Ala	Ser	Leu	Val	Pro	Ala	Ala									
595					600											

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<211> 3003

<212> DNA

<213> unknown

<220>

<223> K:trAPAO

<220>

<221> misc_feature

<222> (73)..(1575)

<223> espl mat

<220>

<221> misc_feature

<222> (1576)..(1611)

<223> spacer sequence

<220>

<221> misc_feature

<222> (1612)..(3000)

<223> K:trAPAO

<220>

<221> CDS

<222> (1)..(3000)

<223>

<220>

<221> misc_feature

<222> (1612)..(1614)

<223> extra lysine

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Met Ala Asn Lys His Leu Ser Leu Ser Leu Phe Leu Val Leu Leu Gly
1 5 10 15

ctc tcc gcc tcc ctc gcc agc ggc gct cct act gtc aag att gat gct 96
Leu Ser Ala Ser Leu Ala Ser Gly Ala Pro Thr Val Lys Ile Asp Ala
20 25 30

ggg atg gtg gtc ggc acg act act act gtc ccc ggc acc act gcg acc 144
Gly Met Val Val Gly Thr Thr Thr Val Pro Gly Thr Thr Ala Thr
35 40 45

gtc agc gag ttc ttg ggc gtt cct ttt gcc gcc tct ccg aca cga ttt 192
Val Ser Glu Phe Leu Gly Val Pro Phe Ala Ala Ser Pro Thr Arg Phe
50 55 60

gcg cct cct act cgt ccc gtg cct tgg tca acg cct ttg caa gcc act 240
Ala Pro Pro Thr Arg Pro Val Pro Trp Ser Thr Pro Leu Gln Ala Thr
65 70 75 80

gca tat ggt oca gca tgc cct caa caa ttc aat tac ccc gaa gaa ctc 288
Ala Tyr Gly Pro Ala Cys Pro Gln Gln Phe Asn Tyr Pro Glu Glu Leu
85 90 95

cgt gag att acg atg gcc tgg ttc aat aca ccg ccc ccg tca gct ggt 336
Arg Glu Ile Thr Met Ala Trp Phe Asn Thr Pro Pro Pro Ser Ala Gly

100	105	110	
gaa agt gag gac tgc ctg aac ctc aac atc tac gtc cca gga act gag Glu Ser Glu Asp Cys Leu Asn Leu Asn Ile Tyr Val Pro Gly Thr Glu 115 120 125			384Glu Ser
aac aca aac aaa gcc gtc atg gtt tgg ata tac ggt gga gcg ctg gaa Asn Thr Asn Lys Ala Val Met Val Trp Ile Tyr Gly Gly Ala Leu Glu 130 135 140			432
tat ggt tgg aat tca ttc cac ctt tac gac ggg gct agt ttc gca gcc Tyr Gly Trp Asn Ser Phe His Leu Tyr Asp Gly Ala Ser Phe Ala Ala 145 150 155 160			480
aat cag gat gtc atc gcc gtg acc atc aac tac aga acg aac att ctg Asn Gln Asp Val Ile Ala Val Thr Ile Asn Tyr Arg Thr Asn Ile Leu 165 170 175			528
ggg ttc cct gct gcc cct cag ctt cca ata aca cag cga aat ctg ggg Gly Phe Pro Ala Ala Pro Gln Leu Pro Ile Thr Gln Arg Asn Leu Gly 180 185 190			576
ttc cta gac caa agg ttt gct ttg gat tgg gta cag cgg aac atc gca Phe Leu Asp Gln Arg Phe Ala Leu Asp Trp Val Gln Arg Asn Ile Ala 195 200 205			624
gcc ttt ggc ggt gat cct cga aag gtc aca ata ttt ggg cag agt gcg Ala Phe Gly Gly Asp Pro Arg Lys Val Thr Ile Phe Gly Gln Ser Ala 210 215 220			672
ggg ggc aga agt gtc gac gtc ctc ttg acg tct atg cca cac aac cca Gly Gly Arg Ser Val Asp Val Leu Leu Thr Ser Met Pro His Asn Pro 225 230 235 240			720
ccc ttc cga gca gca atc atg gag tcc ggt gtg gct aac tac aac ttc Pro Phe Arg Ala Ala Ile Met Glu Ser Gly Val Ala Asn Tyr Asn Phe 245 250 255			768Pro Phe
ccc aag gga gat ttg tcc gaa cct tgg aac acc act gtt caa gct ctc Pro Lys Gly Asp Leu Ser Glu Pro Trp Asn Thr Thr Val Gln Ala Leu 260 265 270			816
aac tgt acc acc agt atc gac atc ttg agt tgt atg aga aga gtc gat Asn Cys Thr Thr Ser Ile Asp Ile Leu Ser Cys Met Arg Arg Val Asp 275 280 285			864
ctc gcc act ctg atg aac acg atc gag caa ctc gga ctt ggg ttt gag Leu Ala Thr Leu Met Asn Thr Ile Glu Gln Leu Gly Leu Gly Phe Glu 290 295 300			912
tac acg ttg gac aac gta acg gct gtg tac cgt tct gaa acg gct cgc Tyr Thr Leu Asp Asn Val Thr Ala Val Tyr Arg Ser Glu Thr Ala Arg 305 310 315 320			960
acg act ggt gac att gct cgt gta cct gtt ctc gtc ggg acg gtg gcc Thr Thr Gly Asp Ile Ala Arg Val Pro Val Leu Val Gly Thr Val Ala 325 330 335			1008

aac gac gga ctt ctc ttt gtc ctc ggg gag aat gac acc caa gca tat Asn Asp Gly Leu Leu Phe Val Leu Gly Glu Asn Asp Thr Gln Ala Tyr 340 345 350	1056
ctc gag gag gca atc ccg aat cag ccc gac ctt tac cag act ctc ctt Leu Glu Glu Ala Ile Pro Asn Gln Pro Asp Leu Tyr Gln Thr Leu Leu 355 360 365	1104
gga gca tat ccc att gga tcc cca ggg atc gga tcg cct caa gat cag Gly Ala Tyr Pro Ile Gly Ser Pro Gly Ile Gly Ser Pro Gln Asp Gln 370 375 380	1152Gly Ala
att gcc gcc att gag acc gag gta aga ttc cag tgt cct tct gcc atc Ile Ala Ala Ile Glu Thr Glu Val Arg Phe Gln Cys Pro Ser Ala Ile 385 390 395 400	1200
gtg gct cag gac tcc cgg aat cgg ggt atc cct tct tgg cgc tac tac Val Ala Gln Asp Ser Arg Asn Arg Gly Ile Pro Ser Trp Arg Tyr Tyr 405 410 415	1248
tac aat gcg acc ttt gag aat ctg gag ctt ttc cct ggg tcc gaa gtg Tyr Asn Ala Thr Phe Glu Asn Leu Glu Leu Phe Pro Gly Ser Glu Val 420 425 430	1296
tac cac agc tct gaa gtc ggg atg gtg ttt ggc acg tat cct gtc gca Tyr His Ser Ser Glu Val Gly Met Val Phe Gly Thr Tyr Pro Val Ala 435 440 445	1344
agt gcg acc gcc ttg gag gcc cag acg agc aaa tac atg cag ggt gcc Ser Ala Thr Ala Leu Glu Ala Gln Thr Ser Lys Tyr Met Gln Gly Ala 450 455 460	1392
tgg gcg gcc ttt gcc aaa aac ccc atg aat ggg cct ggg tgg aaa caa Trp Ala Ala Phe Ala Lys Asn Pro Met Asn Gly Pro Gly Trp Lys Gln 465 470 475 480	1440
gtg ccg aat gtc gcg gcg ctt ggc tca cca ggc aaa gcc atc cag gtt Val Pro Asn Val Ala Ala Leu Gly Ser Pro Gly Lys Ala Ile Gln Val 485 490 495	1488
gac gtc tct cca gcg aca ata gac caa cga tgt gcc ttg tac acg cgt Asp Val Ser Pro Ala Thr Ile Asp Gln Arg Cys Ala Leu Tyr Thr Arg 500 505 510	1536Asp Val
tat tat act gag ttg ggc aca atc gcg ccg agg aca ttt ggc gga ggc Tyr Tyr Thr Glu Leu Gly Thr Ile Ala Pro Arg Thr Phe Gly Gly Gly 515 520 525	1584
agc ggc gga ggc agc ggc gga ggc agc aaa gac aac gtt gcg gac gtg Ser Gly Gly Gly Ser Gly Gly Gly Ser Lys Asp Asn Val Ala Asp Val 530 535 540	1632
gta gtg gtg ggc gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val 545 550 555 560	1680

cag gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val 565 570 575	1728
ggg gga aag act ctg agc gta caa tcg ggt ccc ggc agg acg act atc Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile 580 585 590	1776
aac gac ctc ggc gct gcg tgg atc aat gac agc aac caa agc gaa gta Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val 595 600 605	1824
tcc aga ttg ttt gaa aga ttt cat ttg gag ggc gag ctc cag agg acg Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr 610 615 620	1872
act gga aat tca atc cat caa gca caa gac ggt aca acc act aca gct Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala 625 630 635 640	1920Thr Gly
cct tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala 645 650 655	1968
gaa ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc ctt caa Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln 660 665 670	2016
gac ctc aag gcg agc cct cag gcg aag cgg ctc gac agt gtg agc ttc Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe 675 680 685	2064
gcg cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc ggc gta Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val 690 695 700	2112
gca aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile 705 710 715 720	2160
agc atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt ctc agt Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser 725 730 735	2208
aat att ttc tcg gac aag aaa gac ggc ggg cag tat atg cga tgc aaa Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys 740 745 750	2256
aca ggt atg cag tcg att tgc cat gcc atg tca aag gaa ctt gtt cca Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro 755 760 765	2304Thr Gly
ggc tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag tcg gca Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala 770 775 780	2352
tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa	2400

<211> 1000

<212> PRT

<213> unknown

<220>

<223> K:trAPAO

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<223> espl mat

<220>

<221> misc_feature

<222> (1576)..(1611)

<223> spacer sequence

<220>

<221> misc_feature

<222> (1612)..(3000)

<223> K:trAPAO

<220>

<221> misc_feature

<222> (1612)..(1614)

<223> extra lysine

<400> 25

Met	Ala	Asn	Lys	His	Leu	Ser	Leu	Ser	Leu	Phe	Leu	Val	Leu	Leu	Gly
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Leu	Ser	Ala	Ser	Leu	Ala	Ser	Gly	Ala	Pro	Thr	Val	Lys	Ile	Asp	Ala
			20					25					30		

Gly	Met	Val	Val	Gly	Thr	Thr	Thr	Thr	Val	Pro	Gly	Thr	Thr	Ala	Thr
		35					40					45			

Val Ser Glu Phe Leu Gly Val Pro Phe Ala Ala Ser Pro Thr Arg Phe
 50 55 60

Ala Pro Pro Thr Arg Pro Val Pro Trp Ser Thr Pro Leu Gln Ala Thr
 65 70 75 80

Ala Tyr Gly Pro Ala Cys Pro Gln Gln Phe Asn Tyr Pro Glu Glu Leu
 85 90 95

Arg Glu Ile Thr Met Ala Trp Phe Asn Thr Pro Pro Pro Ser Ala Gly
 100 105 110

Glu Ser Glu Asp Cys Leu Asn Leu Asn Ile Tyr Val Pro Gly Thr Glu
 115 120 125

Asn Thr Asn Lys Ala Val Met Val Trp Ile Tyr Gly Gly Ala Leu Glu
 130 135 140

Tyr Gly Trp Asn Ser Phe His Leu Tyr Asp Gly Ala Ser Phe Ala Ala
 145 150 155 160

Asn Gln Asp Val Ile Ala Val Thr Ile Asn Tyr Arg Thr Asn Ile Leu
 165 170 175

Gly Phe Pro Ala Ala Pro Gln Leu Pro Ile Thr Gln Arg Asn Leu Gly
 180 185 190

Phe Leu Asp Gln Arg Phe Ala Leu Asp Trp Val Gln Arg Asn Ile Ala
 195 200 205

Ala Phe Gly Gly Asp Pro Arg Lys Val Thr Ile Phe Gly Gln Ser Ala
 210 215 220

Gly Gly Arg Ser Val Asp Val Leu Leu Thr Ser Met Pro His Asn Pro
 225 230 235 240

Pro Phe Arg Ala Ala Ile Met Glu Ser Gly Val Ala Asn Tyr Asn Phe
 245 250 255

Pro Lys Gly Asp Leu Ser Glu Pro Trp Asn Thr Thr Val Gln Ala Leu
 260 265 270

Asn Cys Thr Thr Ser Ile Asp Ile Leu Ser Cys Met Arg Arg Val Asp
 275 280 285

Leu Ala Thr Leu Met Asn Thr Ile Glu Gln Leu Gly Leu Gly Phe Glu
 290 295 300

Tyr Thr Leu Asp Asn Val Thr Ala Val Tyr Arg Ser Glu Thr Ala Arg
 305 310 315 320

Thr Thr Gly Asp Ile Ala Arg Val Pro Val Leu Val Gly Thr Val Ala
 325 330 335

Asn Asp Gly Leu Leu Phe Val Leu Gly Glu Asn Asp Thr Gln Ala Tyr
 340 345 350

Leu Glu Glu Ala Ile Pro Asn Gln Pro Asp Leu Tyr Gln Thr Leu Leu
 355 360 365

Gly Ala Tyr Pro Ile Gly Ser Pro Gly Ile Gly Ser Pro Gln Asp Gln
 370 375 380

Ile Ala Ala Ile Glu Thr Glu Val Arg Phe Gln Cys Pro Ser Ala Ile
 385 390 395 400

Val Ala Gln Asp Ser Arg Asn Arg Gly Ile Pro Ser Trp Arg Tyr Tyr
 405 410 415

Tyr Asn Ala Thr Phe Glu Asn Leu Glu Leu Phe Pro Gly Ser Glu Val
 420 425 430

Tyr His Ser Ser Glu Val Gly Met Val Phe Gly Thr Tyr Pro Val Ala
 435 440 445

Ser Ala Thr Ala Leu Glu Ala Gln Thr Ser Lys Tyr Met Gln Gly Ala
 450 455 460

Trp Ala Ala Phe Ala Lys Asn Pro Met Asn Gly Pro Gly Trp Lys Gln
 465 470 475 480

Val Pro Asn Val Ala Ala Leu Gly Ser Pro Gly Lys Ala Ile Gln Val
 485 490 495

Asp Val Ser Pro Ala Thr Ile Asp Gln Arg Cys Ala Leu Tyr Thr Arg
500 505 510

Tyr Tyr Thr Glu Leu Gly Thr Ile Ala Pro Arg Thr Phe Gly Gly Gly
515 520 525

Ser Gly Gly Gly Ser Gly Gly Gly Ser Lys Asp Asn Val Ala Asp Val
530 535 540

Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val
545 550 555 560

Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val
565 570 575

Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile
580 585 590

Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val
595 600 605

Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr
610 615 620

Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala
625 630 635 640

Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala
645 650 655

Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln
660 665 670

Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe
675 680 685

Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val
690 695 700

Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile
705 710 715 720

Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser

725								730				735				
Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly	Gly	Gln	Tyr	Met	Arg	Cys	Lys	
			740					745					750			
Thr	Gly	Met	Gln	Ser	Ile	Cys	His	Ala	Met	Ser	Lys	Glu	Leu	Val	Pro	
		755					760					765				
Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val	Ala	Glu	Ile	Glu	Gln	Ser	Ala	
	770					775					780					
Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser	Gly	Ala	Val	Phe	Arg	Ser	Lys	
785					790					795					800	
Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr	Leu	Tyr	Pro	Thr	Leu	Thr	Phe	
				805					810					815		
Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln	Ala	Leu	Ala	Glu	Asn	Ser	Ile	
			820					825					830			
Leu	Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe	Val	Trp	Asp	Lys	Pro	Trp	Trp	
		835					840					845				
Arg	Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu	Gln	Ser	Ser	Cys	Asp	Pro	Ile	
	850					855					860					
Ser	Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp	Val	Asp	Arg	Gln	Trp	Ser	Ile	
865					870					875					880	
Thr	Cys	Phe	Met	Val	Gly	Asp	Pro	Gly	Arg	Lys	Trp	Ser	Gln	Gln	Ser	
				885					890					895		
Lys	Gln	Val	Arg	Gln	Lys	Ser	Val	Trp	Asp	Gln	Leu	Arg	Ala	Ala	Tyr	
			900					905					910			
Glu	Asn	Ala	Gly	Ala	Gln	Val	Pro	Glu	Pro	Ala	Asn	Val	Leu	Glu	Ile	
		915					920					925				
Glu	Trp	Ser	Lys	Gln	Gln	Tyr	Phe	Gln	Gly	Ala	Pro	Ser	Ala	Val	Tyr	
	930					935					940					
Gly	Leu	Asn	Asp	Leu	Ile	Thr	Leu	Gly	Ser	Ala	Leu	Arg	Thr	Pro	Phe	
945					950					955					960	

Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly
 965 970 975

Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val
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Val Ala Ser Leu Val Pro Ala Ala
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<223> Barley alpha amylase signal sequence

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<222> (73)..()

<223> BEST1 mature

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<222> (1546)..(1584)

<223> spacer sequence

<220>

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<222> (1585)..(2973)

<223> K:trAPAO

<220>

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<222> (1585)..(1587)

<223> Extra lysine

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-20 -15 -10

ctc tcc gcc tcc ctc gcc agc ggc acg gat ttt ccg gtc cgc agg acc 96

Leu Ser Ala Ser Leu Ala Ser Gly Thr Asp Phe Pro Val Arg Arg Thr
-5 -1 1 5

gat ctg ggc cag gtt cag gga ctg gcc ggg gac gtg atg agc ttt cgc 144

Asp Leu Gly Gln Val Gln Gly Leu Ala Gly Asp Val Met Ser Phe Arg
10 15 20

gga ata ccc tat gca gcg ccg ccg gtg ggc ggg ctg cgt tgg aag ccg 192

Gly Ile Pro Tyr Ala Ala Pro Pro Val Gly Gly Leu Arg Trp Lys Pro
25 30 35 40

ccc caa cac gcc cgg ccc tgg gcg ggc gtt cgc ccc gcc acc caa ttt 240

Pro Gln His Ala Arg Pro Trp Ala Gly Val Arg Pro Ala Thr Gln Phe
45 50 55

ggc tcc gac tgc ttc ggc gcg gcc tat ctt cgc aaa ggc agc ctc gcc 288

Gly Ser Asp Cys Phe Gly Ala Ala Tyr Leu Arg Lys Gly Ser Leu Ala
60 65 70

ccc ggc gtg agc gag gac tgt ctt tac ctc aac gta tgg gcg ccg tca Pro Gly Val Ser Glu Asp Cys Leu Tyr Leu Asn Val Trp Ala Pro Ser 75 80 85	336
ggc gct aaa ccc ggc cag tac ccc gtc atg gtc tgg gtc tac ggc ggc Gly Ala Lys Pro Gly Gln Tyr Pro Val Met Val Trp Val Tyr Gly Gly 90 95 100	384
ggc ttc gcc ggc ggc acg gcc gcc atg ccc tac tac gac ggc gag gcg Gly Phe Ala Gly Gly Thr Ala Ala Met Pro Tyr Tyr Asp Gly Glu Ala 105 110 115 120	432
ctt gcg cga cag ggc gtc gtc gtg gtg acg ttt aac tat cgg acg aac Leu Ala Arg Gln Gly Val Val Val Val Thr Phe Asn Tyr Arg Thr Asn 125 130 135	480
atc ctg ggc ttt ttc gcc cat cct ggt ctc tcg cgc gag agc ccc acc Ile Leu Gly Phe Phe Ala His Pro Gly Leu Ser Arg Glu Ser Pro Thr 140 145 150	528
gga act tcg ggc aac tac ggc cta ctc gac att ctc gcc gct ctt cgg Gly Thr Ser Gly Asn Tyr Gly Leu Leu Asp Ile Leu Ala Ala Leu Arg 155 160 165	576
tgg gtg cag agc aac gcc cgc gcc ttc gga ggg gac ccc ggc cga gtg Trp Val Gln Ser Asn Ala Arg Ala Phe Gly Gly Asp Pro Gly Arg Val 170 175 180	624
acg gtc ttt ggt gaa tcg gcc gga gcg agc gcg atc gga ctt ctg ctc Thr Val Phe Gly Glu Ser Ala Gly Ala Ser Ala Ile Gly Leu Leu Leu 185 190 195 200	672
acc tcg ccg ctg agc aag ggt ctc ttc cgt ggc gct atc ctc gaa agt Thr Ser Pro Leu Ser Lys Gly Leu Phe Arg Gly Ala Ile Leu Glu Ser 205 210 215	720
cca ggg ctg acg cga ccg ctc gcg acg ctc gcc gac agc gcc gcc tcg Pro Gly Leu Thr Arg Pro Leu Ala Thr Leu Ala Asp Ser Ala Ala Ser 220 225 230	768
ggc gag cgc ctc gac gcc gat ctt tcg cga ctg cgc tcg acc gac cca Gly Glu Arg Leu Asp Ala Asp Leu Ser Arg Leu Arg Ser Thr Asp Pro 235 240 245	816
gcc acc ctg atg gcg cgc gcc gac gcg gcc cgc ccg gca tcg cgg gac Ala Thr Leu Met Ala Arg Ala Asp Ala Ala Arg Pro Ala Ser Arg Asp 250 255 260	864
ctg cgc agg ccg cgt ccg acc gga ccg atc gtc gat ggc cat gtg ctg Leu Arg Arg Pro Arg Pro Thr Gly Pro Ile Val Asp Gly His Val Leu 265 270 275 280	912
ccg cag acc gac agc gcg gcg atc gcg gcg ggg cag ctg gcg ccg gtt Pro Gln Thr Asp Ser Ala Ala Ile Ala Ala Gly Gln Leu Ala Pro Val 285 290 295	960
cgg gtc ctg atc gga acc aat gcc gac gaa ggc cgc gcc ttc ctc ggg	1008

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cgc	gcg	ccg	atg	gag	acg	cca	gcg	gac	tac	caa	gcc	tat	ctg	gag	gcg	1056	
Arg	Ala	Pro	Met	Glu	Thr	Pro	Ala	Asp	Tyr	Gln	Ala	Tyr	Leu	Glu	Ala		
		315					320				325						
cag	ttt	ggc	gac	caa	gcc	gcc	gcc	gtg	gcg	gcg	tgc	tat	ccc	ctc	gac	1104	
Gln	Phe	Gly	Asp	Gln	Ala	Ala	Ala	Val	Ala	Ala	Cys	Tyr	Pro	Leu	Asp		
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Gly	Arg	Ala	Thr	Pro	Lys	Glu	Met	Val	Ala	Arg	Ile	Phe	Gly	Asp	Asn		
345					350					355					360		
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Gln	Phe	Asn	Arg	Gly	Val	Ser	Ala	Phe	Ser	Glu	Ala	Leu	Val	Arg	Gln		
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Gly	Ala	Pro	Val	Trp	Arg	Tyr	Gln	Phe	Asn	Gly	Asn	Thr	Glu	Gly	Gly		
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Arg	Ala	Pro	Ala	Thr	His	Gly	Ala	Glu	Ile	Pro	Tyr	Val	Phe	Gly	Val		
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ttc	aag	ctc	gac	gag	ttg	ggg	ctg	ttc	gat	tgg	ccg	ccc	gag	ggg	ccc	1344	
Phe	Lys	Leu	Asp	Glu	Leu	Gly	Leu	Phe	Asp	Trp	Pro	Pro	Glu	Gly	Pro		
	410					415					420						
acg	ccc	gcc	gac	cgt	gcg	ctg	ggc	caa	ctg	atg	tcc	tcc	gcc	tgg	gtc	1392	
Thr	Pro	Ala	Asp	Arg	Ala	Leu	Gly	Gln	Leu	Met	Ser	Ser	Ala	Trp	Val		
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cgg	ttc	gcc	aag	aat	ggc	gac	ccc	gcc	ggg	gac	gcc	ctt	acc	tgg	cct	1440	
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gcc	tat	tct	acg	ggc	aag	tcg	acc	atg	aca	ttc	ggg	ccc	gag	ggc	cgc	1488	
Ala	Tyr	Ser	Thr	Gly	Lys	Ser	Thr	Met	Thr	Phe	Gly	Pro	Glu	Gly	Arg		
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gcg	gcg	gtg	gtg	tcg	ccc	gga	cct	tcc	atc	ccc	cct	tgc	gcg	gat	ggc	1536	
Ala	Ala	Val	Val	Ser	Pro	Gly	Pro	Ser	Ile	Pro	Pro	Cys	Ala	Asp	Gly		
		475				480						485					
gcc	aag	gcg	ggg	ggc	gga	ggc	agc	ggc	gga	ggc	agc	ggc	gga	ggc	agc	1584	
Ala	Lys	Ala	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser		
	490					495					500						
aaa	gac	aac	gtt	gcg	gac	gtg	gta	gtg	gtg	ggc	gct	ggc	ttg	agc	ggt	1632	
Lys	Asp	Asn	Val	Ala	Asp	Val	Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly		
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ttg	gag	acg	gca	cgc	aaa	gtc	cag	gcc	gcc	ggg	ctg	tcc	tgc	ctc	gtt	1680	
Leu	Glu	Thr	Ala	Arg	Lys	Val	Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val		

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Gly	Pro	Gly	Arg	Thr	Thr	Ile	Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn					
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Asp	Ser	Asn	Gln	Ser	Glu	Val	Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu					
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Glu	Gly	Glu	Leu	Gln	Arg	Thr	Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln					
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Asp	Gly	Thr	Thr	Thr	Thr	Ala	Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu					
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gag	gtt	gca	agt	gca	ctt	gcg	gaa	ctc	ctc	ccc	gta	tgg	tct	cag	ctg	1968				
Glu	Val	Ala	Ser	Ala	Leu	Ala	Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu					
620										625					630					
atc	gaa	gag	cat	agc	ctt	caa	gac	ctc	aag	gcg	agc	cct	cag	gcg	aag	2016				
Ile	Glu	Glu	His	Ser	Leu	Gln	Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys					
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cgg	ctc	gac	agt	gtg	agc	ttc	gcg	cac	tac	tgt	gag	aag	gaa	cta	aac	2064				
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ttg	cct	gct	gtt	ctc	ggc	gta	gca	aac	cag	atc	aca	cgc	gct	ctg	ctc	2112				
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ggt	gtg	gaa	gcc	cac	gag	atc	agc	atg	ctt	ttt	ctc	acc	gac	tac	atc	2160				
Gly	Val	Glu	Ala	His	Glu	Ile	Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile					
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aag	agt	gcc	acc	ggt	ctc	agt	aat	att	ttc	tcg	gac	aag	aaa	gac	ggc	2208				
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700										705					710					
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715										720					725					
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730										735					740					
gct	gaa	att	gag	cag	tcg	gca	tcc	ggc	tgt	aca	gta	cga	tcg	gcc	tcg	2352				
Ala	Glu	Ile	Glu	Gln	Ser	Ala	Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser					
745										750					755					760

ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc	2400
Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr	
765 770 775	
ttg tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa	2448
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln	
780 785 790	
gca ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc	2496
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe	
795 800 805	
gta tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc	2544
Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu	
810 815 820	
caa tcg agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac	2592
Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp	
825 830 835 840	
gtc gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga	2640
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly	
845 850 855	
cgg aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg	2688
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp	
860 865 870	
gac caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag	2736
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu	
875 880 885	
ccg gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa	2784
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln	
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gga gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt	2832
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly	
905 910 915 920	
tcg gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag	2880
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu	
925 930 935	
acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt	2928
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly	
940 945 950	
caa cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag	2976
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<212> PRT

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<222> (1585)..(1587)

<223> Extra lysine

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Asp Leu Gly Gln Val Gln Gly Leu Ala Gly Asp Val Met Ser Phe Arg
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Gly Ile Pro Tyr Ala Ala Pro Pro Val Gly Gly Leu Arg Trp Lys Pro
25 30 35 40

Pro Gln His Ala Arg Pro Trp Ala Gly Val Arg Pro Ala Thr Gln Phe
 45 50 55

Gly Ser Asp Cys Phe Gly Ala Ala Tyr Leu Arg Lys Gly Ser Leu Ala
60 65 70

Pro Gly Val Ser Glu Asp Cys Leu Tyr Leu Asn Val Trp Ala Pro Ser
75 80 85

Gly Ala Lys Pro Gly Gln Tyr Pro Val Met Val Trp Val Tyr Gly Gly
90 95 100

Gly Phe Ala Gly Gly Thr Ala Ala Met Pro Tyr Tyr Asp Gly Glu Ala
105 110 115 120

Leu Ala Arg Gln Gly Val Val Val Val Thr Phe Asn Tyr Arg Thr Asn
125 130 135

Ile Leu Gly Phe Phe Ala His Pro Gly Leu Ser Arg Glu Ser Pro Thr
140 145 150

Gly Thr Ser Gly Asn Tyr Gly Leu Leu Asp Ile Leu Ala Ala Leu Arg
155 160 165

Trp Val Gln Ser Asn Ala Arg Ala Phe Gly Gly Asp Pro Gly Arg Val
170 175 180

Thr Val Phe Gly Glu Ser Ala Gly Ala Ser Ala Ile Gly Leu Leu Leu
Thr Val Phe Gly Glu Ser Ala Gly Ala Ser Ala Ile Gly Leu Leu Leu
185 190 195 200

Thr Ser Pro Leu Ser Lys Gly Leu Phe Arg Gly Ala Ile Leu Glu Ser
205 210 215

Pro Gly Leu Thr Arg Pro Leu Ala Thr Leu Ala Asp Ser Ala Ala Ser
220 225 230

Gly Glu Arg Leu Asp Ala Asp Leu Ser Arg Leu Arg Ser Thr Asp Pro
235 240 245

Ala Thr Leu Met Ala Arg Ala Asp Ala Ala Arg Pro Ala Ser Arg Asp
250 255 260

Leu Arg Arg Pro Arg Pro Thr Gly Pro Ile Val Asp Gly His Val Leu
265 270 275 280

Pro Gln Thr Asp Ser Ala Ala Ile Ala Ala Gly Gln Leu Ala Pro Val
 285 290 295

Arg Val Leu Ile Gly Thr Asn Ala Asp Glu Gly Arg Ala Phe Leu Gly
 300 305 310

Arg Ala Pro Met Glu Thr Pro Ala Asp Tyr Gln Ala Tyr Leu Glu Ala
 315 320 325

Gln Phe Gly Asp Gln Ala Ala Ala Val Ala Ala Cys Tyr Pro Leu Asp
 330 335 340

Gly Arg Ala Thr Pro Lys Glu Met Val Ala Arg Ile Phe Gly Asp Asn
 345 350 355 360

Gln Phe Asn Arg Gly Val Ser Ala Phe Ser Glu Ala Leu Val Arg Gln
 365 370 375

Gly Ala Pro Val Trp Arg Tyr Gln Phe Asn Gly Asn Thr Glu Gly Gly
 380 385 390

Arg Ala Pro Ala Thr His Gly Ala Glu Ile Pro Tyr Val Phe Gly Val
 395 400 405

Phe Lys Leu Asp Glu Leu Gly Leu Phe Asp Trp Pro Pro Glu Gly Pro
 410 415 420

Thr Pro Ala Asp Arg Ala Leu Gly Gln Leu Met Ser Ser Ala Trp Val
 425 430 435 440

Arg Phe Ala Lys Asn Gly Asp Pro Ala Gly Asp Ala Leu Thr Trp Pro
 445 450 455

Ala Tyr Ser Thr Gly Lys Ser Thr Met Thr Phe Gly Pro Glu Gly Arg
 460 465 470

Ala Ala Val Val Ser Pro Gly Pro Ser Ile Pro Pro Cys Ala Asp Gly
 475 480 485

Ala Lys Ala Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
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Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly

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Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser			
540	545		550
Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn			
555	560		565
Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu			
570	575	580	
Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln			
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Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu			
	605	610	615
Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu			
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Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys			
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Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn			
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Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile			
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Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly			
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly			
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Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala			
	715	720	725
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val			
	730	735	740

Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser
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Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr
 765 770 775

Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln
 780 785 790

Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe
 795 800 805

Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu
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Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp
 825 830 835 840

Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly
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Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp
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Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu
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Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln
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Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly
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Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu
 925 930 935

Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly
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ccc act cga ctt ctt ttg gaa tat ctt gaa gaa aaa tat gaa gag 90
 Pro Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu
 -210 -205 -200

cat ttg tat gag cgc gat gaa ggt gat aaa tgg cga aac aaa aag 135
 His Leu Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys
 -195 -190 -185

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 Phe Glu Leu Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp
 -180 -175 -170

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 Gly Asp Val Lys Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile
 -165 -160 -155

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 Ala Asp Lys His Asn Met Leu Gly Gly Cys Pro Lys Glu Arg Ala
 -150 -145 -140

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 Glu Ile Ser Met Leu Glu Gly Ala Val Leu Asp Ile Arg Tyr Gly
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 Val Ser Arg Ile Ala Tyr Ser Lys Asp Phe Glu Thr Leu Lys Val
 -120 -115 -110

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 Asp Phe Leu Ser Lys Leu Pro Glu Met Leu Lys Met Phe Glu Asp Arg
 -105 -100 -95

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gct atc cca caa att gat aag tac ttg aaa tcc agc aag tat ata gca Ala Ile Pro Gln Ile Asp Lys Tyr Leu Lys Ser Ser Lys Tyr Ile Ala -45 -40 -35 -30			600
tgg cct ttg cag ggc tgg caa gcc acg ttt ggt ggt ggc gac cat cct Trp Pro Leu Gln Gly Trp Gln Ala Thr Phe Gly Gly Gly Asp His Pro -25 -20 -15			648
cca aaa tcg gat ctg gtt ccg cgt gga tcc ccg gaa ttc gct cct act Pro Lys Ser Asp Leu Val Pro Arg Gly Ser Pro Glu Phe Ala Pro Thr -10 -5 -1 1			696
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Gln Arg Asn Leu Gly Phe Leu Asp Gln Arg Phe Ala Leu Asp Trp Val	
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Gln Arg Asn Ile Ala Ala Phe Gly Gly Asp Pro Arg Lys Val Thr Ile	
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Phe Gly Gln Ser Ala Gly Gly Arg Ser Val Asp Val Leu Leu Thr Ser	
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Met Pro His Asn Pro Pro Phe Arg Ala Ala Ile Met Glu Ser Gly Val	
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Ala Asn Tyr Asn Phe Pro Lys Gly Asp Leu Ser Glu Pro Trp Asn Thr	
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Ser Glu Thr Ala Arg Thr Thr Gly Asp Ile Ala Arg Val Pro Val Leu	
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Val Gly Thr Val Ala Asn Asp Gly Leu Leu Phe Val Leu Gly Glu Asn	
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Asp Thr Gln Ala Tyr Leu Glu Glu Ala Ile Pro Asn Gln Pro Asp Leu	
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Tyr Gln Thr Leu Leu Gly Ala Tyr Pro Ile Gly Ser Pro Gly Ile Gly	
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Thr	Thr	Thr	Thr	Ala	Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	Glu	Val		
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gca	agt	gca	ctt	gcg	gaa	ctc	ctc	ccc	gta	tgg	tct	cag	ctg	atc	gaa	2616	
Ala	Ser	Ala	Leu	Ala	Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu	Ile	Glu		
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gag	cat	agc	ctt	caa	gac	ctc	aag	gcg	agc	cct	cag	gcg	aag	cgg	ctc	2664	
Glu	His	Ser	Leu	Gln	Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys	Arg	Leu		
	645					650				655							
gac	agt	gtg	agc	ttc	gcg	cac	tac	tgt	gag	aag	gaa	cta	aac	ttg	cct	2712	
Asp	Ser	Val	Ser	Phe	Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn	Leu	Pro		
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gct	gtt	ctc	ggc	gta	gca	aac	cag	atc	aca	cgc	gct	ctg	ctc	ggc	gtg	2760	
Ala	Val	Leu	Gly	Val	Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu	Gly	Val		
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gaa	gcc	cac	gag	atc	agc	atg	ctt	ttt	ctc	acc	gac	tac	atc	aag	agt	2808	
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Tyr	Met	Arg	Cys	Lys	Thr	Gly	Met	Gln	Ser	Ile	Cys	His	Ala	Met	Ser		
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Lys	Glu	Leu	Val	Pro	Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val	Ala	Glu		
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Ile	Glu	Gln	Ser	Ala	Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser	Gly	Ala		
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Val	Phe	Arg	Ser	Lys	Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr	Leu	Tyr		
		775						780					785				
ccc	acc	ttg	aca	ttt	tca	cca	cct	ctt	ccc	gcc	gag	aag	caa	gca	ttg	3096	
Pro	Thr	Leu	Thr	Phe	Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln	Ala	Leu		
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gcg	gaa	aat	tct	atc	ctg	ggc	tac	tat	agc	aag	ata	gtc	ttc	gta	tgg	3144	
Ala	Glu	Asn	Ser	Ile	Leu	Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe	Val	Trp		
	805					810					815						
gac	aag	ccg	tgg	tgg	cgc	gaa	caa	ggc	ttc	tcg	ggc	gtc	ctc	caa	tcg	3192	
Asp	Lys	Pro	Trp	Trp	Arg	Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu	Gln	Ser		

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Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp	840	845	850	
cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga cgg aag				3288
Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys	855	860	865	
tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg gac caa				3336
Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln	870	875	880	
ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg gcc				3384
Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala	885	890	895	
aac gtg ctc gaa atc gag tgg tgc aag cag cag tat ttc caa gga gct				3432
Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala	900	905	910	915
ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt tcg gcg				3480
Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala	920	925	930	
ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag acg tct				3528
Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser	935	940	945	
tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt caa cga				3576
Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg	950	955	960	
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His Leu Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys
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Phe Glu Leu Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp
      -180                      -175                      -170

Gly Asp Val Lys Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile
      -165                      -160                      -155

Ala Asp Lys His Asn Met Leu Gly Gly Cys Pro Lys Glu Arg Ala
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Glu Ile Ser Met Leu Glu Gly Ala Val Leu Asp Ile Arg Tyr Gly
      -135                      -130                      -125

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Val Ser Arg Ile Ala Tyr Ser Lys Asp Phe Glu Thr Leu Lys Val
-120 -115 -110

Asp Phe Leu Ser Lys Leu Pro Glu Met Leu Lys Met Phe Glu Asp Arg
-105 -100 -95

Leu Cys His Lys Thr Tyr Leu Asn Gly Asp His Val Thr His Pro Asp
-90 -85 -80

Phe Met Leu Tyr Asp Ala Leu Asp Val Val Leu Tyr Met Asp Pro Met
-75 -70 -65

Cys Leu Asp Ala Phe Pro Lys Leu Val Cys Phe Lys Lys Arg Ile Glu
-60 -55 -50

Ala Ile Pro Gln Ile Asp Lys Tyr Leu Lys Ser Ser Lys Tyr Ile Ala
-45 -40 -35 -30

Trp Pro Leu Gln Gly Trp Gln Ala Thr Phe Gly Gly Gly Asp His Pro
-25 -20 -15

Pro Lys Ser Asp Leu Val Pro Arg Gly Ser Pro Glu Phe Ala Pro Thr
-10 -5 -1 1

Val Lys Ile Asp Ala Gly Met Val Val Gly Thr Thr Thr Thr Val Pro
5 10 15

Gly Thr Thr Ala Thr Val Ser Glu Phe Leu Gly Val Pro Phe Ala Ala
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Ser Pro Thr Arg Phe Ala Pro Pro Thr Arg Pro Val Pro Trp Ser Thr
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Pro Leu Gln Ala Thr Ala Tyr Gly Pro Ala Cys Pro Gln Gln Phe Asn
55 60 65

Tyr Pro Glu Glu Leu Arg Glu Ile Thr Met Ala Trp Phe Asn Thr Pro
70 75 80

Pro Pro Ser Ala Gly Glu Ser Glu Asp Cys Leu Asn Leu Asn Ile Tyr
85 90 95

Val Pro Gly Thr Glu Asn Thr Asn Lys Ala Val Met Val Trp Ile Tyr
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Gly Gly Ala Leu Glu Tyr Gly Trp Asn Ser Phe His Leu Tyr Asp Gly
 120 125 130

Ala Ser Phe Ala Ala Asn Gln Asp Val Ile Ala Val Thr Ile Asn Tyr
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Arg Thr Asn Ile Leu Gly Phe Pro Ala Ala Pro Gln Leu Pro Ile Thr
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Gln Arg Asn Leu Gly Phe Leu Asp Gln Arg Phe Ala Leu Asp Trp Val
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Gln Arg Asn Ile Ala Ala Phe Gly Gly Asp Pro Arg Lys Val Thr Ile
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Phe Gly Gln Ser Ala Gly Gly Arg Ser Val Asp Val Leu Leu Thr Ser
 200 205 210

Met Pro His Asn Pro Pro Phe Arg Ala Ala Ile Met Glu Ser Gly Val
 215 220 225

Ala Asn Tyr Asn Phe Pro Lys Gly Asp Leu Ser Glu Pro Trp Asn Thr
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Thr Val Gln Ala Leu Asn Cys Thr Thr Ser Ile Asp Ile Leu Ser Cys
 245 250 255

Met Arg Arg Val Asp Leu Ala Thr Leu Met Asn Thr Ile Glu Gln Leu
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Gly Leu Gly Phe Glu Tyr Thr Leu Asp Asn Val Thr Ala Val Tyr Arg
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Ser Glu Thr Ala Arg Thr Thr Gly Asp Ile Ala Arg Val Pro Val Leu
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Val Gly Thr Val Ala Asn Asp Gly Leu Leu Phe Val Leu Gly Glu Asn
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Asp Thr Gln Ala Tyr Leu Glu Glu Ala Ile Pro Asn Gln Pro Asp Leu

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 Cys Pro Ser Ala Ile Val Ala Gln Asp Ser Arg Asn Arg Gly Ile Pro
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 Ser Trp Arg Tyr Tyr Tyr Asn Ala Thr Phe Glu Asn Leu Glu Leu Phe
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 Pro Gly Ser Glu Val Tyr His Ser Ser Glu Val Gly Met Val Phe Gly
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 Thr Tyr Pro Val Ala Ser Ala Thr Ala Leu Glu Ala Gln Thr Ser Lys
 420 425 430 435
 Tyr Met Gln Gly Ala Trp Ala Ala Phe Ala Lys Asn Pro Met Asn Gly
 440 445 450
 Pro Gly Trp Lys Gln Val Pro Asn Val Ala Ala Leu Gly Ser Pro Gly
 455 460 465
 Lys Ala Ile Gln Val Asp Val Ser Pro Ala Thr Ile Asp Gln Arg Cys
 470 475 480
 Ala Leu Tyr Thr Arg Tyr Tyr Thr Glu Leu Gly Thr Ile Ala Pro Arg
 485 490 495
 Thr Phe Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Lys Asp
 500 505 510 515
 Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu
 520 525 530
 Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu
 535 540 545
 Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro
 550 555 560

Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser
 565 570 575

Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly
 580 585 590 595

Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly
 600 605 610

Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val
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Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu
 630 635 640

Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu
 645 650 655

Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro
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Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val
 680 685 690

Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser
 695 700 705

Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln
 710 715 720

Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met Ser
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Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu
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Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala
 760 765 770

Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr
 775 780 785

Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu
790 795 800

Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp
805 810 815

Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser
820 825 830 835

Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp
840 845 850

Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys
855 860 865

Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln
870 875 880

Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala
885 890 895

Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala
900 905 910 915

Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala
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Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser
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gag att tca atg ctt gaa gga gcg gtt ttg gat att aga tac ggt	315
Glu Ile Ser Met Leu Glu Gly Ala Val Leu Asp Ile Arg Tyr Gly	
-135 -130 -125	
gtt tcg aga att gca tat agt aaa gac ttt gaa act ctc aaa gtt	360
Val Ser Arg Ile Ala Tyr Ser Lys Asp Phe Glu Thr Leu Lys Val	
-120 -115 -110	
gat ttt ctt agc aag cta cct gaa atg ctg aaa atg ttc gaa gat cgt	408
Asp Phe Leu Ser Lys Leu Pro Glu Met Leu Lys Met Phe Glu Asp Arg	
-105 -100 -95	
tta tgt cat aaa aca tat tta aat ggt gat cat gta acc cat cct gac	456
Leu Cys His Lys Thr Tyr Leu Asn Gly Asp His Val Thr His Pro Asp	
-90 -85 -80	
ttc atg ttg tat gac gct ctt gat gtt gtt tta tac atg gac cca atg	504
Phe Met Leu Tyr Asp Ala Leu Asp Val Val Leu Tyr Met Asp Pro Met	
-75 -70 -65	
tgc ctg gat gcg ttc cca aaa tta gtt tgt ttt aaa aaa cgt att gaa	552
Cys Leu Asp Ala Phe Pro Lys Leu Val Cys Phe Lys Lys Arg Ile Glu	

-60	-55	-50	
gct atc cca caa att gat aag tac ttg aaa tcc agc aag tat ata gca			600
Ala Ile Pro Gln Ile Asp Lys Tyr Leu Lys Ser Ser Lys Tyr Ile Ala			
-45	-40	-35	-30
tggttg cct ttg cag ggc ttg caa gcc acg ttt ggt ggt ggc gac cat cct			648
Trp Pro Leu Gln Gly Trp Gln Ala Thr Phe Gly Gly Gly Asp His Pro			
	-25	-20	-15
cca aaa tcg gat ctg gtt ccg cgt gga tcc ccg gaa ttc acg gat ttt			696
Pro Lys Ser Asp Leu Val Pro Arg Gly Ser Pro Glu Phe Thr Asp Phe			
	-10	-5	-1 1
ccg gtc cgc agg acc gat ctg ggc cag gtt cag gga ctg gcc ggg gac			744
Pro Val Arg Arg Thr Asp Leu Gly Gln Val Gln Gly Leu Ala Gly Asp			
5	10	15	
gtg atg agc ttt cgc gga ata ccc tat gca gcg ccg ccg gtg ggc ggg			792
Val Met Ser Phe Arg Gly Ile Pro Tyr Ala Ala Pro Pro Val Gly Gly			
20	25	30	35
ctg cgt tgg aag ccg ccc caa cac gcc cgg ccc tgg gcg ggc gtt cgc			840
Leu Arg Trp Lys Pro Pro Gln His Ala Arg Pro Trp Ala Gly Val Arg			
	40	45	50
ccc gcc acc caa ttt ggc tcc gac tgc ttc ggc gcg gcc tat ctt cgc			888
Pro Ala Thr Gln Phe Gly Ser Asp Cys Phe Gly Ala Ala Tyr Leu Arg			
	55	60	65
aaa ggc agc ctc gcc ccc ggc gtg agc gag gac tgt ctt tac ctc aac			936
Lys Gly Ser Leu Ala Pro Gly Val Ser Glu Asp Cys Leu Tyr Leu Asn			
	70	75	80
gta tgg gcg ccg tca ggc gct aaa ccc ggc cag tac ccc gtc atg gtc			984
Val Trp Ala Pro Ser Gly Ala Lys Pro Gly Gln Tyr Pro Val Met Val			
	85	90	95
tggttg gtc tac ggc ggc ggc ttc gcc ggc ggc acg gcc gcc atg ccc tac			1032
Trp Val Tyr Gly Gly Gly Phe Ala Gly Gly Thr Ala Ala Met Pro Tyr			
100	105	110	115
tac gac ggc gag gcg ctt gcg cga cag ggc gtc gtc gtg gtg acg ttt			1080
Tyr Asp Gly Glu Ala Leu Ala Arg Gln Gly Val Val Val Val Thr Phe			
	120	125	130
aac tat cgg acg aac atc ctg ggc ttt ttc gcc cat cct ggt ctc tcg			1128
Asn Tyr Arg Thr Asn Ile Leu Gly Phe Phe Ala His Pro Gly Leu Ser			
	135	140	145
cgc gag agc ccc acc gga act tcg ggc aac tac ggc cta ctc gac att			1176
Arg Glu Ser Pro Thr Gly Thr Ser Gly Asn Tyr Gly Leu Leu Asp Ile			
	150	155	160
ctc gcc gct ctt cgg tgg gtg cag agc aac gcc cgc gcc ttc gga ggg			1224
Leu Ala Ala Leu Arg Trp Val Gln Ser Asn Ala Arg Ala Phe Gly Gly			
	165	170	175

gac ccc ggc cga gtg acg gtc ttt ggt gaa tcg gcc gga gcg agc gcg Asp Pro Gly Arg Val Thr Val Phe Gly Glu Ser Ala Gly Ala Ser Ala 180 185 190 195	1272
atc gga ctt ctg ctc acc tcg ccg ctg agc aag ggt ctc ttc cgt ggc Ile Gly Leu Leu Leu Thr Ser Pro Leu Ser Lys Gly Leu Phe Arg Gly 200 205 210	1320
gct atc ctc gaa agt cca ggg ctg acg cga ccg ctc gcg acg ctc gcc Ala Ile Leu Glu Ser Pro Gly Leu Thr Arg Pro Leu Ala Thr Leu Ala 215 220 225	1368
gac agc gcc gcc tcg ggc gag cgc ctc gac gcc gat ctt tcg cga ctg Asp Ser Ala Ala Ser Gly Glu Arg Leu Asp Ala Asp Leu Ser Arg Leu 230 235 240	1416
cgc tcg acc gac cca gcc acc ctg atg gcg cgc gcc gac gcg gcc cgc Arg Ser Thr Asp Pro Ala Thr Leu Met Ala Arg Ala Asp Ala Ala Arg 245 250 255	1464
ccg gca tcg cgg gac ctg cgc agg ccg cgt ccg acc gga ccg atc gtc Pro Ala Ser Arg Asp Leu Arg Arg Pro Arg Pro Thr Gly Pro Ile Val 260 265 270 275	1512
gat ggc cat gtg ctg ccg cag acc gac agc gcg gcg atc gcg gcg ggg Asp Gly His Val Leu Pro Gln Thr Asp Ser Ala Ala Ile Ala Ala Gly 280 285 290	1560
cag ctg gcg ccg gtt cgg gtc ctg atc gga acc aat gcc gac gaa ggc Gln Leu Ala Pro Val Arg Val Leu Ile Gly Thr Asn Ala Asp Glu Gly 295 300 305	1608
cgc gcc ttc ctc ggg cgc gcg ccg atg gag acg cca gcg gac tac caa Arg Ala Phe Leu Gly Arg Ala Pro Met Glu Thr Pro Ala Asp Tyr Gln 310 315 320	1656
gcc tat ctg gag gcg cag ttt ggc gac caa gcc gcc gcc gtg gcg gcg Ala Tyr Leu Glu Ala Gln Phe Gly Asp Gln Ala Ala Ala Val Ala Ala 325 330 335	1704
tgc tat ccc ctc gac ggc cgg gcc acg ccc aag gaa atg gtc gcg cgc Cys Tyr Pro Leu Asp Gly Arg Ala Thr Pro Lys Glu Met Val Ala Arg 340 345 350 355	1752
atc ttc ggc gac aat cag ttc aat cgg ggg gtc tcg gcc ttc tcg gaa Ile Phe Gly Asp Asn Gln Phe Asn Arg Gly Val Ser Ala Phe Ser Glu 360 365 370	1800
gcg ctt gtg cgc cag ggc gcg ccc gtg tgg cgt tat cag ttc aac ggt Ala Leu Val Arg Gln Gly Ala Pro Val Trp Arg Tyr Gln Phe Asn Gly 375 380 385	1848
aat acc gag ggt gga aga gcg ccg gct acc cac gga gcc gaa att ccc Asn Thr Glu Gly Gly Arg Ala Pro Ala Thr His Gly Ala Glu Ile Pro 390 395 400	1896

tac gtt ttc ggg gtg ttc aag ctc gac gag ttg ggt ctg ttc gat tgg Tyr Val Phe Gly Val Phe Lys Leu Asp Glu Leu Gly Leu Phe Asp Trp 405 410 415	1944
ccg ccc gag ggg ccc acg ccc gcc gac cgt gcg ctg ggc caa ctg atg Pro Pro Glu Gly Pro Thr Pro Ala Asp Arg Ala Leu Gly Gln Leu Met 420 425 430 435	1992
tcc tcc gcc tgg gtc cgg ttc gcc aag aat ggc gac ccc gcc ggg gac Ser Ser Ala Trp Val Arg Phe Ala Lys Asn Gly Asp Pro Ala Gly Asp 440 445 450	2040
gcc ctt acc tgg cct gcc tat tct acg ggc aag tcg acc atg aca ttc Ala Leu Thr Trp Pro Ala Tyr Ser Thr Gly Lys Ser Thr Met Thr Phe 455 460 465	2088
ggt ccc gag ggc cgc gcg gcg gtg gtg tcg ccc gga cct tcc atc ccc Gly Pro Glu Gly Arg Ala Ala Val Val Ser Pro Gly Pro Ser Ile Pro 470 475 480	2136
cct tgc gcg gat ggc gcc aag gcg ggg ggc gga ggc agc ggc gga ggc Pro Cys Ala Asp Gly Ala Lys Ala Gly Gly Gly Gly Ser Gly Gly Gly 485 490 495	2184
agc ggc gga ggc agc aaa gac aac gtt gcg gac gtg gta gtg gtg ggc Ser Gly Gly Gly Ser Lys Asp Asn Val Ala Asp Val Val Val Val Gly 500 505 510 515	2232
gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc cag gcc gcc ggt Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly 520 525 530	2280
ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta ggg gga aag act Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr 535 540 545	2328
ctg agc gta caa tcg ggt ccc ggc agg acg act atc aac gac ctc ggc Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly 550 555 560	2376
gct gcg tgg atc aat gac agc aac caa agc gaa gta tcc aga ttg ttt Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe 565 570 575	2424
gaa aga ttt cat ttg gag ggc gag ctc cag agg acg act gga aat tca Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser 580 585 590 595	2472
atc cat caa gca caa gac ggt aca acc act aca gct cct tat ggt gac Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp 600 605 610	2520
tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg gaa ctc ctc ccc Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro 615 620 625	2568
gta tgg tct cag ctg atc gaa gag cat agc ctt caa gac ctc aag gcg	2616

Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala	
630 635 640	
agc cct cag gcg aag cgg ctc gac agt gtg agc ttc gcg cac tac tgt	2664
Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys	
645 650 655	
gag aag gaa cta aac ttg cct gct gtt ctc ggc gta gca aac cag atc	2712
Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile	
660 665 670 675	
aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc agc atg ctt ttt	2760
Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Leu Phe	
680 685 690	
ctc acc gac tac atc aag agt gcc acc ggt ctc agt aat att ttc tcg	2808
Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser	
695 700 705	
gac aag aaa gac ggc ggg cag tat atg cga tgc aaa aca ggt atg cag	2856
Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln	
710 715 720	
tcg att tgc cat gcc atg tca aag gaa ctt gtt cca ggc tca gtg cac	2904
Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val His	
725 730 735	
ctc aac acc ccc gtc gct gaa att gag cag tcg gca tcc ggc tgt aca	2952
Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr	
740 745 750 755	
gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt	3000
Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val Val Val	
760 765 770	
tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt tca cca cct ctt	3048
Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu	
775 780 785	
ccc gcc gag aag caa gca ttg gcg gaa aat tct atc ctg ggc tac tat	3096
Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr	
790 795 800	
agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg cgc gaa caa ggc	3144
Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly	
805 810 815	
ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc tca ttt gcc aga	3192
Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg	
820 825 830 835	
gat acc agc atc gac gtc gat cga caa tgg tcc att acc tgt ttc atg	3240
Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met	
840 845 850	
gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc aag cag gta cga	3288
Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg	

855	860	865	
caa aag tct gtc tgg gac caa ctc cgc gca gcc tac gag aac gcc ggg			3336
Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly			
870	875	880	
gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc gag tgg tcg aag			3384
Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys			
885	890	895	
cag cag tat ttc caa gga gct ccg agc gcc gtc tat ggg ctg aac gat			3432
Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp			
900	905	910	915
ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc aag agt gtt cat			3480
Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His			
920	925	930	
ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg tat atg gaa ggg			3528
Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly			
935	940	945	
gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt gtg gct agc ctg			3576
Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu			
950	955	960	
gtg cca gca gca tag			3591
Val Pro Ala Ala			
965			

<210> 31

<211> 1196

<212> PRT

<213> Unknown

<220>

<223> Open reading frame of BEST1:K:trAPAO fusion for bacterial expression vector pGEX-4T-1

<220>

<221> misc_feature

<222> (1)..(687)

<223> gst + polylinker

<220>

<221> misc_feature

<222> (2164)..(2199)

<223> spacer sequence

<220>

<221> misc_feature

<222> (2200)..(3588)

<223> K:trAPAO

<220>

<221> misc_feature

<222> (2200)..(2202)

<223> extra lysine

<400> 31

Met	Ser	Pro	Ile	Leu	Gly	Tyr	Trp	Lys	Ile	Lys	Gly	Leu	Val	Gln
				-225					-220					-215

Pro	Thr	Arg	Leu	Leu	Leu	Glu	Tyr	Leu	Glu	Glu	Lys	Tyr	Glu	Glu
				-210					-205					-200

His	Leu	Tyr	Glu	Arg	Asp	Glu	Gly	Asp	Lys	Trp	Arg	Asn	Lys	Lys
				-195					-190					-185

Phe	Glu	Leu	Gly	Leu	Glu	Phe	Pro	Asn	Leu	Pro	Tyr	Tyr	Ile	Asp
				-180					-175					-170

Gly	Asp	Val	Lys	Leu	Thr	Gln	Ser	Met	Ala	Ile	Ile	Arg	Tyr	Ile
				-165					-160					-155

Ala	Asp	Lys	His	Asn	Met	Leu	Gly	Gly	Cys	Pro	Lys	Glu	Arg	Ala
				-150					-145					-140

Glu	Ile	Ser	Met	Leu	Glu	Gly	Ala	Val	Leu	Asp	Ile	Arg	Tyr	Gly
				-135					-130					-125

Val	Ser	Arg	Ile	Ala	Tyr	Ser	Lys	Asp	Phe	Glu	Thr	Leu	Lys	Val
				-120					-115					-110

Asp	Phe	Leu	Ser	Lys	Leu	Pro	Glu	Met	Leu	Lys	Met	Phe	Glu	Asp	Arg
Asp	Phe	Leu	Ser	Lys	Leu	Pro	Glu	Met	Leu	Lys	Met	Phe	Glu	Asp	Arg
				-105					-100					-95	

Leu Cys His Lys Thr Tyr Leu Asn Gly Asp His Val Thr His Pro Asp
-90 -85 -80

Phe Met Leu Tyr Asp Ala Leu Asp Val Val Leu Tyr Met Asp Pro Met
-75 -70 -65

Cys Leu Asp Ala Phe Pro Lys Leu Val Cys Phe Lys Lys Arg Ile Glu
-60 -55 -50

Ala Ile Pro Gln Ile Asp Lys Tyr Leu Lys Ser Ser Lys Tyr Ile Ala
-45 -40 -35 -30

Trp Pro Leu Gln Gly Trp Gln Ala Thr Phe Gly Gly Gly Asp His Pro
-25 -20 -15

Pro Lys Ser Asp Leu Val Pro Arg Gly Ser Pro Glu Phe Thr Asp Phe
-10 -5 -1 1

Pro Val Arg Arg Thr Asp Leu Gly Gln Val Gln Gly Leu Ala Gly Asp
5 10 15

Val Met Ser Phe Arg Gly Ile Pro Tyr Ala Ala Pro Pro Val Gly Gly
20 25 30 35

Leu Arg Trp Lys Pro Pro Gln His Ala Arg Pro Trp Ala Gly Val Arg
40 45 50

Pro Ala Thr Gln Phe Gly Ser Asp Cys Phe Gly Ala Ala Tyr Leu Arg
55 60 65

Lys Gly Ser Leu Ala Pro Gly Val Ser Glu Asp Cys Leu Tyr Leu Asn
70 75 80

Val Trp Ala Pro Ser Gly Ala Lys Pro Gly Gln Tyr Pro Val Met Val
85 90 95

Trp Val Tyr Gly Gly Gly Phe Ala Gly Gly Thr Ala Ala Met Pro Tyr
100 105 110 115

Tyr Asp Gly Glu Ala Leu Ala Arg Gln Gly Val Val Val Val Thr Phe
120 125 130

Asn Tyr Arg Thr Asn Ile Leu Gly Phe Phe Ala His Pro Gly Leu Ser
135 140 145

Arg Glu Ser Pro Thr Gly Thr Ser Gly Asn Tyr Gly Leu Leu Asp Ile
150 155 160

Leu Ala Ala Leu Arg Trp Val Gln Ser Asn Ala Arg Ala Phe Gly Gly
165 170 175

Asp Pro Gly Arg Val Thr Val Phe Gly Glu Ser Ala Gly Ala Ser Ala
180 185 190 195

Ile Gly Leu Leu Leu Thr Ser Pro Leu Ser Lys Gly Leu Phe Arg Gly
200 205 210

Ala Ile Leu Glu Ser Pro Gly Leu Thr Arg Pro Leu Ala Thr Leu Ala
215 220 225

Asp Ser Ala Ala Ser Gly Glu Arg Leu Asp Ala Asp Leu Ser Arg Leu
230 235 240

Arg Ser Thr Asp Pro Ala Thr Leu Met Ala Arg Ala Asp Ala Ala Arg
245 250 255

Pro Ala Ser Arg Asp Leu Arg Arg Pro Arg Pro Thr Gly Pro Ile Val
260 265 270 275

Asp Gly His Val Leu Pro Gln Thr Asp Ser Ala Ala Ile Ala Ala Gly
280 285 290

Gln Leu Ala Pro Val Arg Val Leu Ile Gly Thr Asn Ala Asp Glu Gly
295 300 305

Arg Ala Phe Leu Gly Arg Ala Pro Met Glu Thr Pro Ala Asp Tyr Gln
310 315 320

Ala Tyr Leu Glu Ala Gln Phe Gly Asp Gln Ala Ala Ala Val Ala Ala
325 330 335

Cys Tyr Pro Leu Asp Gly Arg Ala Thr Pro Lys Glu Met Val Ala Arg
340 345 350 355

Ile Phe Gly Asp Asn Gln Phe Asn Arg Gly Val Ser Ala Phe Ser Glu
360 365 370

Ala Leu Val Arg Gln Gly Ala Pro Val Trp Arg Tyr Gln Phe Asn Gly
375 380 385

Asn Thr Glu Gly Gly Arg Ala Pro Ala Thr His Gly Ala Glu Ile Pro
390 395 400

Tyr Val Phe Gly Val Phe Lys Leu Asp Glu Leu Gly Leu Phe Asp Trp
405 410 415

Pro Pro Glu Gly Pro Thr Pro Ala Asp Arg Ala Leu Gly Gln Leu Met
420 425 430 435

Ser Ser Ala Trp Val Arg Phe Ala Lys Asn Gly Asp Pro Ala Gly Asp
440 445 450

Ala Leu Thr Trp Pro Ala Tyr Ser Thr Gly Lys Ser Thr Met Thr Phe
455 460 465

Gly Pro Glu Gly Arg Ala Ala Val Val Ser Pro Gly Pro Ser Ile Pro
470 475 480

Pro Cys Ala Asp Gly Ala Lys Ala Gly Gly Gly Gly Ser Gly Gly Gly
485 490 495

Ser Gly Gly Gly Ser Lys Asp Asn Val Ala Asp Val Val Val Val Gly
500 505 510 515

Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly
520 525 530

Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr
535 540 545

Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly
550 555 560

Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe
565 570 575

Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser

580		585		590		595
Ile His Gln Ala	Gln Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp	600		605		610
Ser Leu Leu Ser	Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro	615		620		625
Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala		630		635		640
Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys		645		650		655
Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile		660		665		670
Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Leu Phe		680		685		690
Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser		695		700		705
Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln		710		715		720
Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val His		725		730		735
Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr		740		745		750
Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val Val Val		760		765		770
Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu		775		780		785
Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr		790		795		800
Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly		805		810		815

Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg
820 825 830 835

Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met
840 845 850

Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg
855 860 865

Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly
870 875 880

Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys
885 890 895

Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp
900 905 910 915

Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His
920 925 930

Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly
935 940 945

Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu
950 955 960

Val Pro Ala Ala
965

<210> 32

<211> 1803

<212> DNA

<213> Unknown

<220>

<223> Glyc(-) APAO coding sequence; mutation in putative glycosylation sites

<220>

<221> CDS

<222> (1)..(1803)

<223>

<400> 32

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Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Val Ala Ser Pro	
1 5 10 15	

gca ggg tat tct cac gtc ggc gta ggc cca gac gga ggg agg tat gtg	96
Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Gly Arg Tyr Val	
20 25 30	

aca ata gct gga cag att gga caa gac gct tcg ggc gtg aca gac cct	144
Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro	
35 40 45	

gcc tac gag aaa cag gtt gcc caa gca ttc gcc aat ctg cga gct tgc	192
Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys	
50 55 60	

ctt gct gca gtt gga gcc act tca aac gac gtc acc aag ctc aat tac	240
Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr	
65 70 75 80	

tac atc gtc gac tac gcc ccg agc aaa ctc acc gca att gga gat ggg	288
Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly	
85 90 95	

ctg aag gct acc ttt gcc ctt gac agg ctc cct cct tgc acg ctg gtg	336
Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val	
100 105 110	

cca gtg tcg gcc ttg tct tca cct gaa tac ctc ttt gag gtt gat gcc	384
Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala	
115 120 125	

acg gcg ctg gtg ccg gga cac acg acc cca gac aac gtt gcg gac gtg	432
Thr Ala Leu Val Pro Gly His Thr Thr Pro Asp Asn Val Ala Asp Val	
130 135 140	

gta gtg gtg ggc gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc	480
Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val	
145 150 155 160	

cag gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta	528
Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val	
165 170 175	

ggg gga aag act ctg agc gta caa tcg ggt ccc ggc agg acg act atc	576
Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile	

180	185	190	
aac gac ctc ggc gct gcg tgg atc aat gat agc aat cag gcc gaa gta Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ala Glu Val 195 200 205			624
tcc aga ttg ttt gaa aga ttt cat ttg gag ggc gag ctc cag agg acg Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr 210 215 220			672
act gga aat tca atc cat caa gca caa gac ggt aca acc act aca gct Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala 225 230 235 240			720
cct tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala 245 250 255			768
gaa ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc ctt caa Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln 260 265 270			816
gac ctc aag gcg agc cct cag gcg aag cgg ctc gac agt gtg agc ttc Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe 275 280 285			864
gcg cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc ggc gta Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val 290 295 300			912
gca aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile 305 310 315 320			960
agc atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt ctc agt Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser 325 330 335			1008
aat att ttc tcg gac aag aaa gac ggc ggg cag tat atg cga tgc aaa Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys 340 345 350			1056
aca ggt atg cag tcg att tgc cat gcc atg tca aag gaa ctt gtt cca Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro 355 360 365			1104
ggc tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag tcg gca Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala 370 375 380			1152
tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys 385 390 395 400			1200
aag gtg gtg gtt tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe 405 410 415			1248

tca cca cct ctt ccc gcc gag aag caa gca ttg gcg gaa aat tct atc	1296
Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile	
420 425 430	
ctg ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg	1344
Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp	
435 440 445	
cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc	1392
Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile	
450 455 460	
tca ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg tcc att	1440
Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile	
465 470 475 480	
acc tgt ttc atg gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc	1488
Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser	
485 490 495	
aag cag gta cga caa aag tct gtc tgg gac caa ctc cgc gca gcc tac	1536
Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr	
500 505 510	
gag aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc	1584
Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile	
515 520 525	
gag tgg tcg aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat	1632
Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr	
530 535 540	
ggg ctg aac gat ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc	1680
Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe	
545 550 555 560	
aag agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg	1728
Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly	
565 570 575	
tat atg gaa ggg gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt	1776
Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val	
580 585 590	
gtg gct agc ctg gtg cca gca gca tag	1803
Val Ala Ser Leu Val Pro Ala Ala	
595 600	

<210> 33

<211> 600

<212> PRT

<213> Unknown

<220>

<223> Glyc(-) APAO coding sequence; mutation in putative glycosylation sites

<400> 33

Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Val Ala Ser Pro
1 5 10 15

Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Gly Arg Tyr Val
20 25 30

Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro
35 40 45

Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys
50 55 60

Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr
65 70 75 80

Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly
85 90 95

Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val
100 105 110

Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala
115 120 125

Thr Ala Leu Val Pro Gly His Thr Thr Pro Asp Asn Val Ala Asp Val
130 135 140

Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val
145 150 155 160

Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val
165 170 175

Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile
180 185 190

Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ala Glu Val
 195 200 205

Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr
 210 215 220

Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala
 225 230 235 240

Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala
 245 250 255

Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln
 260 265 270

Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe
 275 280 285

Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val
 290 295 300

Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile
 305 310 315 320

Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser
 325 330 335

Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys
 340 345 350

Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro
 355 360 365

Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala
 370 375 380

Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys
 385 390 395 400

Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe
 405 410 415

Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile
420 425 430

Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp
435 440 445

Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile
450 455 460

Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile
465 470 475 480

Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser
485 490 495

Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr
500 505 510

Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile
515 520 525

Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr
530 535 540

Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe
545 550 555 560

Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly
565 570 575

Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val
580 585 590

Val Ala Ser Leu Val Pro Ala Ala
595 600

<210> 34

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> 37-mer oligonucleotide

<400> 34

ggggaattca tggcacttgc accgagctac atcaatc

37

<210> 35

<211> 1929

<212> DNA

<213> *Exophiala spinifera*

<220>

<221> Intron

<222> (739)..(811)

<223>

<220>

<221> Intron

<222> (1134)..(1186)

<223>

<400> 35

atggcacttg caccgagcta catcaatccc ccaaacgtcg cctccccagc aggggtattcc 60

cacatcggcg taggccccaa cgaagcgagg tatgtgacaa tagctggaca gattggacaa 120

gacgcttttg gcgtgacaga cccagcctac gagaaacagg ttgccaagc attcgccaat 180

ctgcgagctt gccttgctgc agttggagcc tcttcaaacg acgtcaccaa gctcaattac 240

tacatcgtcg actacgcccc gagcaaaactc accgcaattg gagatgggct gaagtctacc 300

tttgcccttg acaggctccc tccttgacag ctggtgccag taccggcctt ggcttcacct 360

gaatacctct ttgaggttga tgccacggcg ctggtgccag gacactcgac cccagacaac 420

gttgcgagcg tggtagtggt gggcgctggc ttgagcggtt tggagacggc acgcaaagtc 480

caggccgccc gtctgtcctg cctcgttctt gaggcgatgg atcgtgtagg gggaaagact 540

ctgagcgtac aatcgggtcc cggcaggacg actatcaacg acctcggcgc tgcgtggatc	600
aatgacagca accaaagcga agtatccaga ttgtttgaaa gatttcattt ggagggcgag	660
ctccagagga cgaccggaaa ttcaatccat caagcacaag acggtacaac cactacagct	720
ccttatggtg actccccggt aagcacaatc ccactttgtg atgagacctc tgtcgagtgt	780
agaatacagt cactgactcc acttcgtcca gctgagcgag gaggttgcaa gtgcacttgc	840
ggaactcctc cccgtatggt ctgagctgat cgaagagtat agccttgaag accccaaggc	900
gagccctcag gcgaagcggc tcgacagtgt gagcttcgcg cactactgtg agaaggacct	960
aaacttgctt gctgttctca gcgtggcaaa ccagatcaca cgcgctctgc tcggtgtgga	1020
agcccacgag atcagcatgc tttttctcac cgactacatc aagagtgcc a cgggtctcag	1080
taatattgtc tcggacaaga aagacggcgg gcagtatatg cgatgcaaaa caggtgcgtg	1140
cgggtgcctc tcaggtaggg gactcgtttc ttagtggtca ttccaggtat gcagtcgatt	1200
tgccatgcca tgtcaaagga acttgttcca ggctcagtgc acctcaacac ccccgctcgt	1260
ggaattgagc agtcggcgtc cggctgtata gtacgatcgg cctcggggcg cgtgttccga	1320
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cctcttcccg ccgagaagca agcattggcg gaaaaatcta tcctcggcta ctatagcaag	1440
atagtcttcg tatgggacaa cccgtggtgg cgcaacaag gcttctcggg cgtcctccaa	1500
tcgagctgtg accccatctc atttgccaga gataccagca tcgaagtcca tcggcaatgg	1560
tccattacct gtttcattgt cggagacccg ggacggaagt ggtcccaaca gtccaagcag	1620
gtacgacaaa agtctgtctg ggaccaactc cgcgcagcct acgagaacgc cggggcccaa	1680
gtcccagagc cggccaacgt gctcgaaatc gagtggtcga agcagcagta tttccaagga	1740
gctccgagcg ccgtctatgg gctgaacgat ctcatcacac tgggttcggc gtcagaacg	1800
ccgttcaagt gtgttcattt cgttgaacg gagacgtctt tagtttgga agggatatg	1860
gaaggggcca tacgatcggg tcaacgaggt gctgcagaag ttgtggctag cctggtgcca	1920
gcagcatag	1929

<210> 36

<211> 600

<212> PRT

<213> *Exophilia spinifera*

<400> 36

Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Val Ala Ser Pro
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Ala Gly Tyr Ser His Ile Gly Val Gly Pro Asn Glu Ala Arg Tyr Val
20 25 30

Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Leu Gly Val Thr Asp Pro
35 40 45

Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys
50 55 60

Leu Ala Ala Val Gly Ala Ser Ser Asn Asp Val Thr Lys Leu Asn Tyr
65 70 75 80

Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly
85 90 95

Leu Lys Ser Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val
100 105 110

Pro Val Pro Ala Leu Ala Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala
115 120 125

Thr Ala Leu Val Pro Gly His Ser Thr Pro Asp Asn Val Ala Asp Val
130 135 140

Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val
145 150 155 160

Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val
165 170 175

Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile
180 185 190

Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val
195 200 205

Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr
 210 215 220
 Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala
 225 230 235 240
 Pro Tyr Gly Asp Ser Pro Leu Ser Glu Glu Val Ala Ser Ala Leu Ala
 245 250 255
 Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu Tyr Ser Leu Glu
 260 265 270
 Asp Pro Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe
 275 280 285
 Ala His Tyr Cys Glu Lys Asp Leu Asn Leu Pro Ala Val Leu Ser Val
 290 295 300
 Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile
 305 310 315 320
 Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser
 325 330 335
 Asn Ile Val Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys
 340 345 350
 Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro
 355 360 365
 Gly Ser Val His Leu Asn Thr Pro Val Ala Gly Ile Glu Gln Ser Ala
 370 375 380
 Ser Gly Cys Ile Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys
 385 390 395 400
 Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe
 405 410 415
 Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Lys Ser Ile
 420 425 430
 Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Asn Pro Trp Trp

435		440		445
Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile				
450		455		460
Ser Phe Ala Arg Asp Thr Ser Ile Glu Val Asp Arg Gln Trp Ser Ile				
465		470		475
				480
Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser				
	485		490	495
Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr				
	500		505	510
Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile				
515		520		525
Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr				
530		535		540
Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe				
545		550		555
				560
Lys Cys Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly				
	565		570	575
Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val				
	580		585	590
Val Ala Ser Leu Val Pro Ala Ala				
595		600		

<210> 37

<211> 1929

<212> DNA

<213> *Exophiala spinifera*

<220>

<221> Intron

<222> (739)..(811)

<223>

<220>

<221> Intron

<222> (1134)..(1186)

<223>

<400> 37
atggcacttg caccgagcta catcaatccc ccaaacgtcg cctccccagc agggatttcc 60
cacatcggcg taggccccaa cgaagcgagg tatgtgacaa tagctggaca gattggacaa 120
gacgcttttg gcgtgacaga cccagcctac gagaaacagg ttgcccaagc attcgccaat 180
ctgcgagctt gccttgctgc agttggagcc tcttcaaacg acgtcaccaa gctcaattac 240
tacatcgtcg actacgcccc gagcaaactc accgcaattg gagatgggct gaagtctacc 300
tttgcccttg acaggctccc tccttgcaag ctggtgccag taccggcctt ggcttcacct 360
gaatacctct ttgaggttga cgccacggcg ctggtgccag gacactcgac cccagacaac 420
gttgcgagcg tggtagtggt gggcgctggc ttgagcggct tggagacggc acgcaaagtc 480
caggccgccg gtctgtcctg cctcgttctt gaggcgatgg atcgtgtagg gggaaagact 540
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aatgacagca accaaagcga agtatccaga ttgtttgaaa gatttcattt ggagggcgag 660
ctccagagga cgaccgaaa ttcaatccat caagcacaag acggtacaac cactacagct 720
ccttatggtg actccccggt aagcacaatc ccactttgtg atgagacctc tgtcgagtg 780
agaatacagt cactgactcc acttcgtcca gctgagcgag gaggttgcaa gtgcacttgc 840
agaatacagt cactgactcc acttcgtcca gctgagcgag gaggttgcaa gtgcacttgc 840
ggaactcctc cccgtatggt ctgagctgat cgaagagtat agccttgaag accccaaggc 900
gagccctcag gcgaagcggc tcgacagtgt gagcttcgcg cactactgtg agaaggacct 960
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agccacagag atcagcatgc tttttctcac cgactacatc aagagtgcca ccggtctcag 1080
taatattgtc tcggacaaga aagacggcgg gcagtatatg cgatgcaaaa caggtgcgtg 1140
cgggtgtcctc tcaggtaggg gactcgtttc ttagtgggtca ttccaggat gcagtcgatt 1200

tgccatgcca tgtcaaagga acttggtcca ggctcagtgc acotcaacac cccggtcgct 1260
 ggaattgagc agtcggcgtc cggctgtata gtacgatcgg cctcggggcgc cgtgttccga 1320
 agcaaaaagg tgggtggtttc gttaccgaca acattgtatc ccaccttgac attttcacca 1380
 cctcttccccg ccgagaagca agcattggcg gaaaaatcta tcctcggcta ctatagcaag 1440
 atagtcttcg tatgggacaa cccgtggtgg cgccaacaag gcttctcggg cgtcctccaa 1500
 tcgagctgtg accccatctc atttgccaga gataccagca tcgaagtcga tcggcaatgg 1560
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 gtcccagagc cggccaacgt gctcgaaatc gagtggtcga agcagcagta tttccaagga 1740
 gctccgagcg ccgtctatgg gctgaacgat ctcacacac tgggttcggc gtcagaacg 1800
 ccgttcaagt gtgttcattt cgttggaacg gagacgtctt tagtttggaa agggatatg 1860
 gaaggggcca tacgatcggg tcaacgaggt gctgcagaag ttgtggctag cctggtgcc 1920
 gcagcatag 1929

<210> 38

<211> 600

<212> PRT

<213> *Exophiala spinifera*

<400> 38

Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Val Ala Ser Pro
 1 5 10 15

Ala Gly Tyr Ser His Ile Gly Val Gly Pro Asn Glu Ala Arg Tyr Val
 20 25 30

Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Leu Gly Val Thr Asp Pro
 35 40 45

Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys
 50 55 60

Leu Ala Ala Val Gly Ala Ser Ser Asn Asp Val Thr Lys Leu Asn Tyr
 65 70 75 80

Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly
 85 90 95

Leu Lys Ser Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val
 100 105 110

Pro Val Pro Ala Leu Ala Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala
 115 120 125

Thr Ala Leu Val Pro Gly His Ser Thr Pro Asp Asn Val Ala Asp Val
 130 135 140

Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val
 145 150 155 160

Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val
 165 170 175

Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile
 180 185 190

Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val
 195 200 205

Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr
 210 215 220

Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala
 225 230 235 240

Pro Tyr Gly Asp Ser Pro Leu Ser Glu Glu Val Ala Ser Ala Leu Ala
 245 250 255

Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu Tyr Ser Leu Glu
 260 265 270

Asp Pro Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe
 275 280 285

Ala His Tyr Cys Glu Lys Asp Leu Asn Leu Pro Ala Val Leu Ser Val
 290 295 300

Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile
 305 310 315 320

Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser
 325 330 335

Asn Ile Val Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys
 340 345 350

Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro
 355 360 365

Gly Ser Val His Leu Asn Thr Pro Val Ala Gly Ile Glu Gln Ser Ala
 370 375 380

Ser Gly Cys Ile Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys
 385 390 395 400

Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe
 405 410 415

Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Lys Ser Ile
 420 425 430

Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Asn Pro Trp Trp
 435 440 445

Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile
 450 455 460

Ser Phe Ala Arg Asp Thr Ser Ile Glu Val Asp Arg Gln Trp Ser Ile
 465 470 475 480

Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser
 485 490 495

Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr
 500 505 510

Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile
 515 520 525

Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr
530 535 540

Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe
545 550 555 560

Lys Cys Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly
565 570 575

Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val
580 585 590

Val Ala Ser Leu Val Pro Ala Ala
595 600

<210> 39

<211> 1930

<212> DNA

<213> *Exophiala spinifera*

<220>

<221> Intron

<222> (739)..(811)

<223>

<220>

<221> Intron

<222> (1134)..(1187)

<223>

<220>

<221> misc_feature

<222> (649)..(649)

<223> n = A,T,C or G

<400> 39

atggcacttg caccgagcta catcaatccc ccaaacgtcg cctccccagc agggatttct	60
cacgtcggcg taggcccaga cggagggagg tatgtgacaa tagctggaca gattggacaa	120
gacgcttcgg gcgtgacaga ccctgcctac gagaaacagg ttgcccaagc attcgccaat	180
ctgcgagctt gccttgctgc agttggagcc acttcaaacg acgtcaccaa gctcaattac	240
tacatcgtcg actacgcccc gagcaaactc accgcaattg gagatgggct gaaggctacc	300
tttgcccttg acaggctccc tccttgcaag ctggtgccag tgtcggcctt gtcttcacct	360
gaatacctct ttgaggttga tgccacggcg ctggtgccgg gacacacgac ccagacaac	420
gttgcgagcg tggtagtggt gggcgctggc ttgagcgggt tggagacggc acgcaaagtc	480
caggccgccg gtctgtcctg cctcgcttctt gaggcgatgg atcgtgtagg gggaaagact	540
ctgagcgtac aatcgggtcc cggcaggacg actatcaacg acctcggcgc tgcgtggatc	600
aatgacagca accaaagcga agtatccaga ttgtttgaaa gatttcatnt ggagggcgag	660
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ccttatggtg actccttggt aagcacaatc ccactttgtg atgagacctc tgtcgagtgt	780
agaatacagt cactgattcc acttcgtcca gctgagcgag gaggttgcaa gtgcacttgc	840
ggaactcctc cccgtatggt ctgagctgat cgaagagcat agccttcaag acctcaaggc	900
gagccctcag gcgaagcggc tcgacagtgt gagcttcgcg cactactgtg agaaggaact	960
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taatattttc tcggacaaga aagacggcgg gcagtatatg cgatgcaaaa caggtgcgtg	1140
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gatagtcttc gtatgggaca agccgtggtg gcgcgaacaa ggcttctcgg gcgtcctcca	1500
atcgagctgt gaccccatct catttgccag agataccagc atcgacgtcg atcgacaatg	1560
gtccattacc tgtttcatgg tcggagaccc gggacggaag tgggcccaac agtccaagca	1620

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 gccgttcaag agtggttcatt tcgttggaaac ggagacgtct ttagtttgga aagggtatat 1860
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<210> 40

<211> 598

<212> PRT

<213> *Exophiala spinifera*

<220>

<221> MISC_FEATURE

<222> (216)..(216)

<223> Xaa = any amino acid

<400> 40

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Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro
 35 40 45

Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys
 50 55 60

Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr
 65 70 75 80

Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly

85										90					95				
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Pro	Val	Ser	Ala	Leu	Ser	Ser	Pro	Glu	Tyr	Leu	Phe	Glu	Val	Asp	Ala				
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Thr	Ala	Leu	Val	Pro	Gly	His	Thr	Thr	Pro	Asp	Asn	Val	Ala	Asp	Val				
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Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	Leu	Glu	Ala	Met	Asp	Arg	Val	Gly				
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Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly	Pro	Gly	Arg	Thr	Thr	Ile	Asn				
		180						185					190						
Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp	Ser	Asn	Gln	Ser	Glu	Val	Ser				
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Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys	Arg	Leu	Asp	Ser	Val	Ser	Phe	Ala				
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His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn	Leu	Pro	Ala	Val	Leu	Gly	Val	Asn				
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Gln	Ile	Thr	Arg	Ala	Leu	Leu	Gly	Val	Glu	Ala	His	Glu	Ile	Ser	Met				
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Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile
 325 330 335

Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly
 340 345 350

Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser
 355 360 365

Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly
 370 375 380

Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val
 385 390 395 400

Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro
 405 410 415

Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly
 420 425 430

Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu
 435 440 445

Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe
 450 455 460

Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys
 465 470 475 480

Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln
 485 490 495

Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn
 500 505 510

Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp
 515 520 525

Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu
 530 535 540

Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser
 545 550 555 560

Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met
 565 570 575

Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala
 580 585 590

Ser Leu Val Pro Ala Ala
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<210> 41

<211> 1928

<212> DNA

<213> *Rhinocycladiella atrovirens*

<220>

<221> Intron

<222> (739)..(811)

<223>

<220>

<221> Intron

<222> (1134)..(1185)

<223>

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 ctgcgagctt gtcttgctgc agttggagcc acttcaaacg acattaccaa gctcaattac 240
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cagcatag	1928

<210> 42

<211> 598

<212> PRT

<213> Rhinocycladiella atrovirens

<400> 42

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Ala Gly Tyr Ser His Val Gly Val Gly Pro Asn Gly Gly Arg Tyr Ala
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Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Ala Val Thr Asp Pro
35 40 45

Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys
50 55 60

Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Ile Thr Lys Leu Asn Tyr
65 70 75 80

Tyr Ile Val Asp Tyr Asn Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly
85 90 95

Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val
100 105 110

Pro Val Pro Ala Leu Ala Ser Pro Glu Tyr Pro Phe Glu Val Asp Ala
115 120 125

Thr Ala Leu Val Pro Gly His Ser Thr Pro Asp Asn Val Ala Asp Val
130 135 140

Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val
145 150 155 160

Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val
165 170 175

Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Ala Ile
 180 185 190

Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val
 195 200 205

Phe Lys Leu Phe Glu Arg Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly
 210 215 220

Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro Tyr
 225 230 235 240

Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu
 245 250 255

Leu Pro Ala Trp Ser Gln Leu Ile Glu Glu His Ser Leu Glu Asp Pro
 260 265 270

Lys Ala Ser Pro Gln Ala Lys Gln Leu Asp Ser Val Ser Phe Ala His
 275 280 285

Tyr Cys Glu Lys Asp Leu Ser Leu Pro Ala Val Leu Gly Val Ala Asn
 290 295 300

Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met
 305 310 315 320

Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile
 325 330 335

Val Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly
 340 345 350

Met Gln Ser Leu Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser
 355 360 365

Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly
 370 375 380

Cys Thr Val Arg Ser Ala Ser Gly Gly Val Phe Arg Ser Lys Lys Val
 385 390 395 400

Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Ile Phe Ser Pro

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Gln	Ala	Leu	Ala	Glu	Lys
	425				
Ser	Ile	Leu	Gly		
	430				
Tyr	Tyr	Ser	Lys	Ile	Val
	435				
Phe	Val	Trp	Asp	Lys	Pro
	440				
Trp	Trp	Arg	Glu		
	445				
Gln	Gly	Phe	Ser	Gly	Val
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Leu	Gln	Ser	Ser	Cys	Asp
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Pro	Ile	Ser	Phe		
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Ala	Arg	Asp	Thr	Ser	Ile
	465				
Glu	Val	Asp	Arg	Gln	Trp
	470				
Ser	Ile	Thr	Cys		
	475				
Phe	Met	Val	Gly	Asp	Pro
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	490				
Gln	Gln	Ser	Lys	Gln	
	495				
Val	Arg	Gln	Lys	Ser	Val
	500				
Trp	Asn	Gln	Leu	Arg	Ala
	505				
Ala	Ala	Tyr	Glu	Asn	
	510				
Ala	Gly	Ala	Gln	Val	Pro
	515				
Glu	Pro	Ala	Asn	Val	Leu
	520				
Glu	Ile	Glu	Trp		
	525				
Ser	Lys	Gln	Gln	Tyr	Phe
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Gln	Gly	Ala	Pro	Ser	Val
	535				
Val	Val	Tyr	Gly	Leu	
	540				
Asn	Cys	Leu	Asn	Thr	Leu
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Pro	Phe	Lys	Gly		
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Val	His	Phe	Val	Gly	Thr
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Glu	Thr	Ser	Leu	Val	Trp
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Lys	Gly	Tyr	Met		
	575				
Glu	Gly	Ala	Ile	Arg	Ser
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Val	Val	Ala			
	590				
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<210> 43

<211> 1928

<212> DNA

<213> Rhinocycladiella atrovirens

<220>

<221> Intron

<222> (739)..(811)

<223>

<220>

<221> Intron

<222> (1134)..(1186)

<223>

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gagccctcaa gcgaagcagc tcgacagtgt gagcttcgca cactactgtg agaaggatct 960


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cagcatag 1928

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<210> 44

<211> 591

<212> PRT

<213> *Rhinocycladiella atrovirens*

<400> 44

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Ala Gly Tyr Ser Tyr Val Gly Val Gly Pro Asn Gly Gly Arg Tyr Val
20           25           30

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Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Ala Val Thr Asp Pro
35           40           45

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Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys
50 55 60

Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Ile Thr Lys Leu Asn Tyr
65 70 75 80

Tyr Ile Val Asp Tyr Asn Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly
85 90 95

Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val
100 105 110

Pro Val Pro Ala Leu Ala Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala
115 120 125

Thr Ala Leu Val Pro Gly His Ser Thr Pro Asp Asn Val Ala Asp Val
130 135 140

Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val
145 150 155 160

Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val
165 170 175

Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Gly Arg Thr Thr Ile Asn
180 185 190

Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Lys
195 200 205

Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly
210 215 220

Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro Tyr
225 230 235 240

Gly Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu
245 250 255

Pro Ala Ser Gln Leu Ile Glu Glu His Ser Leu Glu Asp Pro Lys Ala
260 265 270

Ser Pro Gln Ala Lys Gln Leu Asp Ser Val Ser Phe Ala His Tyr Cys
275 280 285

Glu Lys Leu Asn Leu Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg
290 295 300

Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Phe Phe Leu Thr
305 310 315 320

Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Val Ser Asp Lys
325 330 335

Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Leu
340 345 350

Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn
355 360 365

Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg
370 375 380

Ser Ala Ser Gly Gly Val Phe Arg Ser Lys Lys Val Val Leu Pro Thr
385 390 395 400

Leu Tyr Pro Thr Leu Ile Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln
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Ala Leu Ala Glu Lys Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe
420 425 430

Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu
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Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Glu
450 455 460

Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly
465 470 475 480

Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp
485 490 495

Asn Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu
500 505 510

Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln
515 520 525

Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Cys Leu Asn Thr Leu Gly
530 535 540

Ser Ala Leu Arg Thr Pro Phe Lys Gly Val His Phe Val Gly Thr Glu
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<210> 45

<211> 1928

<212> DNA

<213> Rhinocycladiella atrovirens

<220>

<221> Intron

<222> (739)..(811)

<223>

<220>

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<222> (1134)..(1185)

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tcccagagcc ggccaacgtg ctgagatcg agtggtcgaa gcagcagtat ttccaaggag	1740
cgccgagcgc cgtctatggg ctgaactgtc tcaacacact gggttcggcg ctcagaacgc	1800

cgttcaaggg tgttcatttc gttggaacgg agacgtcttt ggtttggaaa gggatatatgg 1860
aagggggccat acgatcgggt cagcgaggcg ctgcagaagt tgtgcctagc ctggtgccag 1920
cagcatag 1928

<210> 46

<211> 591

<212> PRT

<213> Rhinocycladiella atrovirens

<400> 46

Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Ala Ser Pro Ala
1 5 10 15

Gly Tyr Ser His Val Gly Val Gly Pro Asn Gly Gly Arg Tyr Val Thr
20 25 30

Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Ala Val Thr Asp Pro Ala
35 40 45

Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys Leu
Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys Leu
50 55 60

Ala Ala Val Gly Ala Thr Ser Asn Asp Ile Thr Lys Leu Asn Tyr Tyr
65 70 75 80

Ile Val Asp Tyr Asn Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly Leu
85 90 95

Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val Pro
100 105 110

Val Pro Ala Leu Ala Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala Thr
115 120 125

Ala Leu Val Pro Gly His Ser Thr Pro Asp Asn Val Ala Asp Val Val
130 135 140

Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln

145	150	155	160
Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly	165	170	175
Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn	180	185	190
Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Phe	195	200	205
Lys Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr	210	215	220
Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro	225	230	235
Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu	245	250	255
Leu Leu Pro Ala Trp Ser Gln Leu Ile Glu Glu His Ser Leu Glu Asp	260	265	270
Pro Lys Ala Ser Pro Gln Ala Lys Gln Leu Asp Ser Val Ser Phe Ala	275	280	285
His Tyr Cys Glu Lys Asp Leu Asn Leu Pro Ala Val Leu Gly Val Ala	290	295	300
Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser	305	310	315
Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn	325	330	335
Ile Val Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr	340	345	350
Gly Met Gln Ser Leu Cys His Ala Met Ser Lys Glu Leu Val Pro Gly	355	360	365
Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser	370	375	380

Gly Cys Thr Val Arg Ser Ala Ser Gly Gly Val Phe Arg Ser Lys Lys
 385 390 395 400

Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Ile Phe Ser Pro Leu
 405 410 415

Pro Ala Glu Lys Gln Ala Leu Ala Glu Lys Ser Ile Gly Tyr Tyr Ser
 420 425 430

Lys Ile Val Phe Val Asp Lys Leu Trp Trp Arg Glu Gln Gly Phe Ser
 435 440 445

Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr
 450 455 460

Ser Ile Glu Val Asp Arg Gln Ser Ile Thr Cys Phe Met Val Gly Asp
 465 470 475 480

Pro Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val
 485 490 495

Trp Asn Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro
 500 505 510

Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe
 515 520 525

Gln Ala Pro Ser Ala Val Tyr Gly Leu Asn Cys Leu Asn Thr Leu Gly
 530 535 540

Ser Ala Leu Arg Thr Pro Phe Lys Gly Val His Phe Val Gly Thr Glu
 545 550 555 560

Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly
 Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly
 565 570 575

Gln Arg Gly Ala Ala Glu Val Val Pro Ser Leu Val Pro Ala Ala
 580 585 590

<210> 47

<211> 600

<212> PRT

<213> *Exophiala spinifera*

<400> 47

Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Val Ala Ser Pro
1 5 10 15

Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Gly Arg Tyr Val
20 25 30

Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro
35 40 45

Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys
50 55 60

Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr
65 70 75 80

Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly
85 90 95

Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val
100 105 110

Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala
115 120 125

Thr Ala Leu Val Pro Gly His Thr Thr Pro Asp Asn Val Ala Asp Val
130 135 140

Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val
145 150 155 160

Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val
165 170 175

Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile
180 185 190

Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val
 195 200 205

Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr
 210 215 220

Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala
 225 230 235 240

Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala
 245 250 255

Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln
 260 265 270

Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe
 275 280 285

Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val
 290 295 300

Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile
 305 310 315 320

Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser
 Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser
 325 330 335

Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys
 340 345 350

Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro
 355 360 365

Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala
 370 375 380

Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys
 385 390 395 400

Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe
 405 410 415

Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile

420	425	430
Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp		
435	440	445
Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile		
450	455	460
Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile		
465	470	475
Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser		
485	490	495
Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr		
500	505	510
Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile		
515	520	525
Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr		
530	535	540
Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe		
545	550	555
Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly		
565	570	575
Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val		
580	585	590
Val Ala Ser Leu Val Pro Ala Ala		
595	600	

<210> 48

<211> 1392

<212> DNA

<213> Unknown

<220>

<223> Cys (-) APAO; removal of cysteine 461

<220>

<221> CDS

<222> (1)..(1392)

<223>

<400> 48

aaa	gac	aac	gtt	gcg	gac	gtg	gta	gtg	gtg	ggc	gct	ggc	ttg	agc	ggg	48
Lys	Asp	Asn	Val	Ala	Asp	Val	Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly	
1				5					10					15		

ttg	gag	acg	gca	cgc	aaa	gtc	cag	gcc	gcc	ggg	ctg	tcc	tgc	ctc	gtt	96
Leu	Glu	Thr	Ala	Arg	Lys	Val	Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	
			20					25					30			

ctt	gag	gcg	atg	gat	cgt	gta	ggg	gga	aag	act	ctg	agc	gta	caa	tcg	144
Leu	Glu	Ala	Met	Asp	Arg	Val	Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	
		35					40					45				

ggg	ccc	ggc	agg	acg	act	atc	aac	gac	ctc	ggc	gct	gcg	tgg	atc	aat	192
Gly	Pro	Gly	Arg	Thr	Thr	Ile	Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	
	50					55					60					

gac	agc	aac	caa	agc	gaa	gta	tcc	aga	ttg	ttt	gaa	aga	ttt	cat	ttg	240
Asp	Ser	Asn	Gln	Ser	Glu	Val	Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu	
65					70					75					80	

gag	ggc	gag	ctc	cag	agg	acg	act	gga	aat	tca	atc	cat	caa	gca	caa	288
Glu	Gly	Glu	Leu	Gln	Arg	Thr	Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	
				85					90					95		

gac	ggg	aca	acc	act	aca	gct	cct	tat	ggg	gac	tcc	ttg	ctg	agc	gag	336
Asp	Gly	Thr	Thr	Thr	Thr	Ala	Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	
			100					105					110			

gag	gtt	gca	agt	gca	ctt	gcg	gaa	ctc	ctc	ccc	gta	tgg	tct	cag	ctg	384
Glu	Val	Ala	Ser	Ala	Leu	Ala	Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu	
		115					120					125				

atc	gaa	gag	cat	agc	ctt	caa	gac	ctc	aag	gcg	agc	cct	cag	gcg	aag	432
Ile	Glu	Glu	His	Ser	Leu	Gln	Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys	
	130					135					140					

cgg	ctc	gac	agt	gtg	agc	ttc	gcg	cac	tac	tgt	gag	aag	gaa	cta	aac	480
Arg	Leu	Asp	Ser	Val	Ser	Phe	Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn	
145					150					155					160	

ttg	cct	gct	gtt	ctc	ggc	gta	gca	aac	cag	atc	aca	cgc	gct	ctg	ctc	528
Leu	Pro	Ala	Val	Leu	Gly	Val	Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu	

165										170					175					
ggt	gtg	gaa	gcc	cac	gag	atc	agc	atg	ctt	ttt	ctc	acc	gac	tac	atc	576				
Gly	Val	Glu	Ala	His	Glu	Ile	Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile					
			180						185				190							
aag	agt	gcc	acc	ggt	ctc	agt	aat	att	ttc	tcg	gac	aag	aaa	gac	ggc	624				
Lys	Ser	Ala	Thr	Gly	Leu	Ser	Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly					
		195					200					205								
ggg	cag	tat	atg	cga	tgc	aaa	aca	ggt	atg	cag	tcg	att	tgc	cat	gcc	672				
Gly	Gln	Tyr	Met	Arg	Cys	Lys	Thr	Gly	Met	Gln	Ser	Ile	Cys	His	Ala					
	210					215					220									
atg	tca	aag	gaa	ctt	gtt	cca	ggc	tca	gtg	cac	ctc	aac	acc	ccc	gtc	720				
Met	Ser	Lys	Glu	Leu	Val	Pro	Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val					
225					230					235					240					
gct	gaa	att	gag	cag	tcg	gca	tcc	ggc	tgt	aca	gta	cga	tcg	gcc	tcg	768				
Ala	Glu	Ile	Glu	Gln	Ser	Ala	Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser					
			245						250					255						
ggc	gcc	gtg	ttc	cga	agc	aaa	aag	gtg	gtg	gtt	tcg	tta	cgc	aca	acc	816				
Gly	Ala	Val	Phe	Arg	Ser	Lys	Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr					
			260					265					270							
ttg	tat	ccc	acc	ttg	aca	ttt	tca	cca	cct	ctt	ccc	gcc	gag	aag	caa	864				
Leu	Tyr	Pro	Thr	Leu	Thr	Phe	Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln					
		275					280					285								
gca	ttg	gcg	gaa	aat	tct	atc	ctg	ggc	tac	tat	agc	aag	ata	gtc	ttc	912				
Ala	Leu	Ala	Glu	Asn	Ser	Ile	Leu	Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe					
	290					295					300									
gta	tgg	gac	aag	ccg	tgg	tgg	cgc	gaa	caa	ggc	ttc	tcg	ggc	gtc	ctc	960				
Val	Trp	Asp	Lys	Pro	Trp	Trp	Arg	Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu					
305					310					315				320						
caa	tcg	agc	tcc	gac	ccc	atc	tca	ttt	gcc	aga	gat	acc	agc	atc	gac	1008				
Gln	Ser	Ser	Ser	Asp	Pro	Ile	Ser	Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp					
				325					330					335						
gtc	gat	cga	caa	tgg	tcc	att	acc	tgt	ttc	atg	gtc	gga	gac	ccg	gga	1056				
Val	Asp	Arg	Gln	Trp	Ser	Ile	Thr	Cys	Phe	Met	Val	Gly	Asp	Pro	Gly					
			340					345					350							
cgg	aag	tgg	tcc	caa	cag	tcc	aag	cag	gta	cga	caa	aag	tct	gtc	tgg	1104				
Arg	Lys	Trp	Ser	Gln	Gln	Ser	Lys	Gln	Val	Arg	Gln	Lys	Ser	Val	Trp					
		355					360					365								
gac	caa	ctc	cgc	gca	gcc	tac	gag	aac	gcc	ggg	gcc	caa	gtc	cca	gag	1152				
Asp	Gln	Leu	Arg	Ala	Ala	Tyr	Glu	Asn	Ala	Gly	Ala	Gln	Val	Pro	Glu					
	370					375					380									
ccg	gcc	aac	gtg	ctc	gaa	atc	gag	tgg	tcg	aag	cag	cag	tat	ttc	caa	1200				
Pro	Ala	Asn	Val	Leu	Glu	Ile	Glu	Trp	Ser	Lys	Gln	Gln	Tyr	Phe	Gln					
385					390					395					400					

gga gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt 1248
 Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly
 405 410 415

tcg gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag 1296
 Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu
 420 425 430

acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt 1344
 Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly
 435 440 445

caa cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag 1392
 Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
 450 455 460

<210> 49

<211> 463

<212> PRT

<213> Unknown

<220>

<223> Cys (-) APAO; removal of cysteine 461

<400> 49

Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly
 1 5 10 15

Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val
 20 25 30

Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser
 35 40 45

Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn
 50 55 60

Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu
 65 70 75 80

Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln
 85 90 95

Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu
100 105 110

Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu
115 120 125

Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys
130 135 140

Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn
145 150 155 160

Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu
165 170 175

Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile
180 185 190

Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly
195 200 205

Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala
210 215 220

Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val
225 230 235 240

Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser
245 250 255

Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr
260 265 270

Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln
275 280 285

Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe
290 295 300

Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu
305 310 315 320

Gln Ser Ser Ser Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp
325 330 335

Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly
340 345 350

Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp
355 360 365

Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu
370 375 380

Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln
385 390 395 400

Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly
405 410 415

Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu
420 425 430

Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly
435 440 445

Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
450 455 460

<210> 50

<211> 1392

<212> DNA

<213> Unknown

<220>

<223> Cys (-) APAO; removal of cysteines 359 and 461

<220>

<221> CDS

<222> (1)..(1392)

<223>

<400> 50

aaa gac aac gtt gcg gac gtg gta gtg gtg ggc gct ggc ttg agc ggt	48
Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly	
1 5 10 15	
ttg gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt	96
ttg gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt	96
Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val	
20 25 30	
ctt gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg	144
Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser	
35 40 45	
ggt ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat	192
Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn	
50 55 60	
gac agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg	240
Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu	
65 70 75 80	
gag ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa	288
Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln	
85 90 95	
gac ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag	336
Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu	
100 105 110	
gag gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg	384
Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu	
115 120 125	
atc gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag	432
Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys	
130 135 140	
cgg ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac	480
cgg ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac	480
Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn	
145 150 155 160	
ttg cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc	528
Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu	
165 170 175	
ggt gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc	576
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile	
180 185 190	
aag agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc	624
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly	
195 200 205	
ggg cag tat atg cga tgc aaa aca ggt atg cag tcg att tcg cat gcc	672

Gly	Gln	Tyr	Met	Arg	Cys	Lys	Thr	Gly	Met	Gln	Ser	Ile	Ser	His	Ala		
210						215					220						
atg	tca	aag	gaa	ctt	gtt	cca	ggc	tca	gtg	cac	ctc	aac	acc	ccc	gtc	720	
Met	Ser	Lys	Glu	Leu	Val	Pro	Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val		
225					230					235					240		
gct	gaa	att	gag	cag	tcg	gca	tcc	ggc	tgt	aca	gta	cga	tcg	gcc	tcg	768	
Ala	Glu	Ile	Glu	Gln	Ser	Ala	Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser		
				245					250					255			
ggc	gcc	gtg	ttc	cga	agc	aaa	aag	gtg	gtg	gtt	tcg	tta	ccg	aca	acc	816	
Gly	Ala	Val	Phe	Arg	Ser	Lys	Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr		
		260						265				270					
ttg	tat	ccc	acc	ttg	aca	ttt	tca	cca	cct	ctt	ccc	gcc	gag	aag	caa	864	
ttg	tat	ccc	acc	ttg	aca	ttt	tca	cca	cct	ctt	ccc	gcc	gag	aag	caa	864	
Leu	Tyr	Pro	Thr	Leu	Thr	Phe	Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln		
		275					280					285					
gca	ttg	gcg	gaa	aat	tct	atc	ctg	ggc	tac	tat	agc	aag	ata	gtc	ttc	912	
Ala	Leu	Ala	Glu	Asn	Ser	Ile	Leu	Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe		
	290					295					300						
gta	tgg	gac	aag	ccg	tgg	tgg	cgc	gaa	caa	ggc	ttc	tcg	ggc	gtc	ctc	960	
Val	Trp	Asp	Lys	Pro	Trp	Trp	Arg	Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu		
305					310					315					320		
caa	tcg	agc	tcc	gac	ccc	atc	tca	ttt	gcc	aga	gat	acc	agc	atc	gac	1008	
Gln	Ser	Ser	Ser	Asp	Pro	Ile	Ser	Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp		
				325					330					335			
gtc	gat	cga	caa	tgg	tcc	att	acc	tgt	ttc	atg	gtc	gga	gac	ccg	gga	1056	
Val	Asp	Arg	Gln	Trp	Ser	Ile	Thr	Cys	Phe	Met	Val	Gly	Asp	Pro	Gly		
			340					345					350				
cgg	aag	tgg	tcc	caa	cag	tcc	aag	cag	gta	cga	caa	aag	tct	gtc	tgg	1104	
Arg	Lys	Trp	Ser	Gln	Gln	Ser	Lys	Gln	Val	Arg	Gln	Lys	Ser	Val	Trp		
		355					360					365					
gac	caa	ctc	cgc	gca	gcc	tac	gag	aac	gcc	ggg	gcc	caa	gtc	cca	gag	1152	
Asp	Gln	Leu	Arg	Ala	Ala	Tyr	Glu	Asn	Ala	Gly	Ala	Gln	Val	Pro	Glu		
	370					375					380						
ccg	gcc	aac	gtg	ctc	gaa	atc	gag	tgg	tcg	aag	cag	cag	tat	ttc	caa	1200	
Pro	Ala	Asn	Val	Leu	Glu	Ile	Glu	Trp	Ser	Lys	Gln	Gln	Tyr	Phe	Gln		
385					390					395				400			
gga	gct	ccg	agc	gcc	gtc	tat	ggg	ctg	aac	gat	ctc	atc	aca	ctg	ggg	1248	
gga	gct	ccg	agc	gcc	gtc	tat	ggg	ctg	aac	gat	ctc	atc	aca	ctg	ggg	1248	
Gly	Ala	Pro	Ser	Ala	Val	Tyr	Gly	Leu	Asn	Asp	Leu	Ile	Thr	Leu	Gly		
				405				410					415				
tcg	gcg	ctc	aga	acg	ccg	ttc	aag	agt	gtt	cat	ttc	gtt	gga	acg	gag	1296	
Ser	Ala	Leu	Arg	Thr	Pro	Phe	Lys	Ser	Val	His	Phe	Val	Gly	Thr	Glu		
			420				425					430					
acg	tct	tta	gtt	tgg	aaa	ggg	tat	atg	gaa	ggg	gcc	ata	cga	tcg	ggg	1344	
Thr	Ser	Leu	Val	Trp	Lys	Gly	Tyr	Met	Glu	Gly	Ala	Ile	Arg	Ser	Gly		

435	440	445	
caa cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag			1392
Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala			
450	455	460	

<210> 51

<211> 463

<212> PRT

<213> Unknown

<220>

<223> Cys (-) APAO; removal of cysteines 359 and 461

<400> 51

Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly
1 5 10 15

Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val
20 25 30

Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser
35 40 45

Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn
50 55 60

Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu
65 70 75 80

Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln
85 90 95

Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu
100 105 110

Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu
115 120 125

Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys
130 135 140

Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn
 145 150 155 160

Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu
 165 170 175

Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile
 180 185 190

Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly
 195 200 205

Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Ser His Ala
 210 215 220

Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val
 225 230 235 240

Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser
 245 250 255

Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr
 260 265 270

Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln
 275 280 285

Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe
 290 295 300

Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu
 305 310 315 320

Gln Ser Ser Ser Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp
 325 330 335

Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly
 340 345 350

Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp
 355 360 365

Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu
 370 375 380

Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln
 385 390 395 400

Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly
 405 410 415

Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu
 420 425 430

Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly
 435 440 445

Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
 450 455 460

<210> 52

<211> 1392

<212> DNA

<213> Unknown

<220>

<223> Cys (-) APAO; removal of cysteines 169, 359, and 461

<220>

<221> CDS

<222> (1)..(1392)

<223>

<400> 52
 aaa gac aac gtt gcg gac gtg gta gtg gtg ggc gct ggc ttg agc ggt 48
 Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly
 1 5 10 15
 ttg gag acg gca cgc aaa gtc cag gcc gcc ggt ctg agc tcc ctc gtt 96
 Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Ser Leu Val
 20 25 30

ctt gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser 35 40 45	144
ggc ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn 50 55 60	192
gac agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu 65 70 75 80	240
gag ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln 85 90 95	288
gac ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu 100 105 110	336
gag gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu 115 120 125	384
atc gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys 130 135 140	432
cgg ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn 145 150 155 160	480
ttg cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu 165 170 175	528
ggc gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile 180 185 190	576
aag agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly 195 200 205	624
ggg cag tat atg cga tgc aaa aca ggt atg cag tcg att tcg cat gcc Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Ser His Ala 210 215 220	672
atg tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val 225 230 235 240	720
gct gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser 245 250 255	768

ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc	816
Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr	
260 265 270	
ttg tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa	864
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln	
275 280 285	
gca ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc	912
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe	
290 295 300	
gta tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc	960
Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu	
305 310 315 320	
caa tcg agc tcc gac ccc atc tca ttt gcc aga gat acc agc atc gac	1008
Gln Ser Ser Ser Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp	
325 330 335	
gtc gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga	1056
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly	
340 345 350	
cgg aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg	1104
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp	
355 360 365	
gac caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag	1152
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu	
370 375 380	
ccg gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa	1200
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln	
385 390 395 400	
gga gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt	1248
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly	
405 410 415	
tcg gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag	1296
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu	
420 425 430	
acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt	1344
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly	
435 440 445	
caa cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag	1392
Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala	
450 455 460	

<210> 53

<211> 463

<212> PRT

<213> Unknown

<220>

<223> Cys (-) APAO; removal of cysteines 169, 359, and 461

<400> 53

Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly
1 5 10 15

Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Ser Leu Val
20 25 30

Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser
35 40 45

Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn
50 55 60

Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu
65 70 75 80

Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln
85 90 95

Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu
100 105 110

Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu
115 120 125

Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys
130 135 140

Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn
145 150 155 160

Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu
165 170 175

Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile

180	185	190
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly		
195	200	205
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Ser His Ala		
210	215	220
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val		
225	230	235
Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser		
245	250	255
Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr		
260	265	270
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln		
275	280	285
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe		
290	295	300
Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu		
305	310	315
Gln Ser Ser Ser Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp		
325	330	335
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly		
340	345	350
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp		
355	360	365
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu		
370	375	380
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln		
385	390	395
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly		
405	410	415

Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu
 420 425 430

Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly
 435 440 445

Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
 450 455 460

<210> 54

<211> 11

<212> PRT

<213> *Exophiala spinifera*

<400> 54

Asp Val Val Val Val Gly Ala Gly Leu Ser Gly
 1 5 10